

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:52:05 ; Search time 35 Seconds
(without alignments)
597.724 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKSLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:*

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| 2: | /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:* |
| 3: | /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:* |
| 4: | /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:* |
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| 7: | /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:* |
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| 21: | /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:* |
| 22: | /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:* |
| 23: | /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------------------|
| 1 | 811 | 99.9 | 157 | 19 | AAW77077 Human interleukin |
| 2 | 811 | 99.9 | 157 | 21 | AAW57570 Human interleukin |
| 3 | 811 | 99.9 | 157 | 22 | AAE06661 Human interleukin |
| 4 | 811 | 99.9 | 157 | 22 | AAG65294 Human interleukin |
| 5 | 811 | 99.9 | 157 | 22 | AAG65351 Human interleukin |
| 6 | 811 | 99.9 | 157 | 23 | ABB04389 Human IL-18. Homo |
| 7 | 811 | 99.9 | 157 | 23 | AAE16954 Human active inter |
| 8 | 811 | 99.9 | 157 | 23 | AAE17134 Human IL-18 protei |
| 9 | 811 | 99.9 | 158 | 21 | AAW85167 Human interleukin |
| 10 | 811 | 99.9 | 180 | 19 | AAW48959 Wild-type human in |

ALIGNMENTS

RESULT 1

AAW77077 standard; peptide; 157 AA.

ID AAW77077;

AC AAW77077;

XX 16-NOV-1998 (first entry)

DT Human interleukin 18.

DE Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

XX Human; osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.

KW Homo sapiens.

OS EP861663-A2.

PN 02-SEP-1998.

PD 24-FEB-1998; 98EP-0301352.

PF 25-FEB-1997; 97JP-0055468.

PR (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI: 1998-448964/39.

DR N-PSDB; AAV48226.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment

PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,

| | | | | | | |
|----|-----|------|------|----|----------|--------------------|
| 11 | 811 | 99.9 | 193 | 18 | AAW22047 | Interferon gamma i |
| 12 | 811 | 99.9 | 193 | 19 | AAW46592 | Amino acid sequenc |
| 13 | 811 | 99.9 | 193 | 22 | AAB30541 | A human IL-18 with |
| 14 | 811 | 99.9 | 193 | 22 | AAG63830 | Amino acid sequenc |
| 15 | 811 | 99.9 | 193 | 23 | AAE16953 | Human precursor in |
| 16 | 811 | 99.9 | 233 | 23 | AAE16959 | Ubiquitin-human in |
| 17 | 811 | 99.9 | 536 | 23 | AAE16957 | Human pro-IL-18/ca |
| 18 | 811 | 99.9 | 588 | 23 | AAE16958 | Human pro-IL-18/ca |
| 19 | 811 | 99.9 | 1048 | 23 | AAE16960 | Ubiquitin-human in |
| 20 | 810 | 99.8 | 157 | 17 | AAE16960 | Human interferon-g |
| 21 | 810 | 99.8 | 157 | 17 | AAE16958 | Human mature inter |
| 22 | 810 | 99.8 | 157 | 18 | AAW15701 | Interferon-gamma i |
| 23 | 810 | 99.8 | 157 | 18 | AAW24258 | Human protein for |
| 24 | 810 | 99.8 | 157 | 19 | AAW77158 | Human interleukin- |
| 25 | 810 | 99.8 | 157 | 19 | AAW63810 | Human IL-18 protei |
| 26 | 810 | 99.8 | 157 | 19 | AAW37741 | IFN-gamma inducing |
| 27 | 810 | 99.8 | 157 | 19 | AAW52176 | Interferon-gamma i |
| 28 | 810 | 99.8 | 157 | 20 | AAW39799 | Interleukin-18 rec |
| 29 | 810 | 99.8 | 157 | 21 | AAW44597 | Human interleukin- |
| 30 | 810 | 99.8 | 157 | 21 | AAW53904 | Sequence of a matu |
| 31 | 810 | 99.8 | 157 | 22 | AAW82408 | Human interleukin- |
| 32 | 810 | 99.8 | 157 | 22 | AAW89560 | Human interferon-g |
| 33 | 810 | 99.8 | 193 | 19 | AAW37740 | Interferon-gamma i |
| 34 | 810 | 99.8 | 193 | 19 | AAW52172 | Interferon-gamma p |
| 35 | 810 | 99.8 | 193 | 19 | AAW47429 | Interferon-gamma i |
| 36 | 810 | 99.8 | 193 | 21 | AAW53908 | Amino acid sequenc |
| 37 | 810 | 99.8 | 193 | 22 | AAW82409 | Human interleukin- |
| 38 | 808 | 99.5 | 193 | 19 | AAW77082 | Interleukin 18 act |
| 39 | 803 | 98.9 | 193 | 18 | AAW31757 | Interferon gamma i |
| 40 | 801 | 98.6 | 157 | 19 | AAW77083 | Human interleukin |
| 41 | 801 | 98.6 | 157 | 19 | AAW48961 | Mutant human inter |
| 42 | 801 | 98.6 | 181 | 21 | AAW23797 | Human interleukin |
| 43 | 792 | 97.5 | 193 | 22 | AAW72608 | Macaca cynomolgus |
| 44 | 791 | 97.4 | 157 | 19 | AAW77084 | Human interleukin |
| 45 | 791 | 97.4 | 157 | 19 | AAW77085 | Human interleukin |

PT osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
 PT primary hyperthyroidism and osteoporosis
 XX
 PS Claim 4; Page 18; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 XX Sequence 157 AA;
 SQ
 Query Match 99.9%; Score 811; DB 19; Length 157;
 Best Local Similarity 99.4%; Pred. No. 7.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISWKDSQPRGM 60
 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISWKDSQPRGM 60
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
 Db 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 QY 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 Db 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 RESULT 2
 AAY57570
 ID AAY57570 standard; protein; 157 AA.
 XX
 AC AAY57570;
 XX
 DT 06-MAR-2000 (first entry)
 DE Human interleukin 18 protein sequence SEQ ID NO:1.
 XX
 XX Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;
 KW interferon-gamma-inducing factor; growth inhibition; cytostatic.
 KW
 XX Homo sapiens.
 OS
 XX WO959565-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX 20-MAY-1999; 99WO-US111160.
 PF
 XX 21-MAY-1998; 98US-0086560.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Johnson RK;
 PI
 XX WPI; 2000-062368/05.
 DR
 XX New polypeptides, useful for preparation of composition for preventing
 PT and/or treating cancer by inhibiting tumor growth
 PT
 XX Claim 1; Page 49-50; 53pp; English.
 PS
 XX The present sequence represents human interleukin 18 (IL-18). The
 CC present invention describes a compound comprising human or murine IL-18
 CC in combination with a chemotherapeutic agent (I). Also described are:
 CC (1) a method of preventing and/or treating cancer in a mammal comprising
 CC the administration of a cancer inhibiting amount of (I) comprising the
 CC IL-18 protein and the chemotherapeutic agent and optionally a
 CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the
 CC growth of tumour cells in a mammal sensitive to a composition comprising

CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
 CC optionally a pharmaceutically acceptable carrier), comprising
 CC administering to a mammal afflicted with the tumour cells an effective
 CC tumour cell growth inhibiting amount of (I). The IL-18 protein in
 CC conjunction with a chemotherapeutic agent is useful in a method for
 CC preventing and/or treating cancer in mammals by inhibiting the growth
 CC of tumours or cancerous cells in mammals.
 XX
 XX Sequence 157 AA;
 SQ
 Query Match 99.9%; Score 811; DB 21; Length 157;
 Best Local Similarity 99.4%; Pred. No. 7.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISWKDSQPRGM 60
 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISWKDSQPRGM 60
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISWKDSQPRGM 60
 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNAPRTIFIISWKDSQPRGM 60
 QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSDIIFQKSVPGHDKMKQFESSY 120
 Db 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 QY 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 Db 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELDGDRSIMFTVQNE 157
 RESULT 3
 AAE06661
 ID AAE06661 standard; protein; 157 AA.
 XX
 AC AAE06661;
 XX
 DT 16-OCT-2001 (first entry)
 DE Human interleukin-1gamma (IL-1gamma) protein.
 XX
 XX Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
 KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
 KW
 XX Homo sapiens.
 OS
 XX WO200157219-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 01-FEB-2001; 2001WO-US03285.
 PF
 XX 02-FEB-2000; 2000US-0179638.
 PR
 XX (SCHE) SCHERING CORP.
 PA
 XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
 PI
 XX WPI; 2001-488886/53.
 DR
 XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
 PT polypeptide useful for treating conditions exhibiting abnormal
 PT expression of interleukin such as immunological disorders, tumor and
 PT allergy
 PT
 XX Disclosure; Fig 1; 103pp; English.
 PS
 XX The invention relates to recombinant antigenic interleukin-1 like
 CC molecules and their corresponding nucleic acid sequences, designated
 CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
 CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumours, inflammatory diseases, fever, hypoglycaemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as

CC HIV). The invention also relates to methods of using the composition
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
 CC utilities. IL-1delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-1delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is human
 CC interleukin-1gamma (IL-1gamma) protein related to the invention.
 XX
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
 Best Local Similarity 99.4%; Pred. No. 7.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 QY 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIDKTSDIFFQRSVPGHDKMKQFESSY 120
 DB 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIDKTSDIFFQRSVPGHDKMKQFESSY 120
 QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 4
 AAG65294
 ID AAG65294 standard; protein; 157 AA.
 AC AAG65294;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nontropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 9; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a

CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
 Best Local Similarity 99.4%; Pred. No. 7.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
 QY 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIDKTSDIFFQRSVPGHDKMKQFESSY 120
 DB 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIDKTSDIFFQRSVPGHDKMKQFESSY 120
 QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
 DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 5
 AAG65351
 ID AAG65351 standard; protein; 157 AA.
 XX
 AC AAG65351;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) protein fragment.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nontropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Disclosure; Page 14; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The

CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX
 SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 22; Length 157;
 Best Local Similarity 99.4%; Pred. No. 7.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNPRTFIISMYKDSQPRGM 60
 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNPRTFIISMYKDSQPRGM 60
 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSIIFFQSVPGHDKMKQFESSY 120
 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSIIFFQSVPGHDKMKQFESSY 120
 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 6
 ABB04389
 ID ABB04389 standard; protein; 157 AA.
 AC ABB04389;
 21-MAY-2002 (first entry)
 Human IL-18.
 Human; IL-18; Interleukin-18; cancer.
 Homo sapiens.
 CN1326992-A.
 19-DEC-2001.
 07-JUN-2000; 2000CN-0107993.
 07-JUN-2000; 2000CN-0107993.

(SHUA-) SHUANGLU PHARM CO LTD BEIJING.
 Xu M, Wang Y, Huang X;
 WPI; 2002-217571/28.
 N-PSDB; ABL41315.
 Gene cloning, product preparation and use of Chinese interleukin-18
 subtype (53 Arg IL-18), useful for treating of cancer and other disease
 Claim 1; Page 7 (disclosure); 8pp; Chinese.
 The invention relates to the preparation of recombinant human
 Interleukin-18 for treating of cancer and other disease.
 Sequence 157 AA;

Query Match 99.9%; Score 811; DB 23; Length 157;
 Best Local Similarity 99.4%; Pred. No. 7.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNPRTFIISMYKDSQPRGM 60
 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCRDNPRTFIISMYKDSQPRGM 60
 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSIIFFQSVPGHDKMKQFESSY 120
 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDKSIIFFQSVPGHDKMKQFESSY 120
 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 7
 AAE16954
 ID AAE16954 standard; Protein; 157 AA.
 AC AAE16954;
 18-APR-2002 (first entry)
 Human active Interleukin-18 (IL-18) protein.
 Human; Interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;
 Immunocompetent.
 Homo sapiens.
 WO200198455-A2.
 27-DEC-2001.
 11-JUN-2001; 2001WO-US18804.
 15-JUN-2000; 2000US-211832P.
 10-AUG-2000; 2000US-224128P.
 20-JAN-2001; 2001US-264923P.
 (SMIK) SMITHKLINE BEECHAM CORP.

Johanson KO, Kirkpatrick RB, Shatzman AR, Ho YS, Mcdevitt P;
 WPI; 2002-139786/18.
 Activation of precursor polypeptide e.g. interleukin-18 polypeptide
 useful for inducing interferon-gamma production, comprises contacting
 or co-expressing caspase 4 or caspase 5 with precursor polypeptide -
 Claim 9; Fig 3; 64pp; English.
 The invention relates to a method for the in vitro activation of human
 precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
 method comprises contacting precursor IL-18 with an activating enzyme
 such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
 of cysteine proteases that include interleukin-beta converting enzyme
 (ICE), which preferentially cleave substrates containing a protease
 activation motif. The methods are useful for producing physiologically
 active polypeptide e.g. active IL-18 polypeptide. The active IL-18
 polypeptide has an activity of inducing the production of interferon
 (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
 biologically active substance for stimulating the production of IFN-g
 from KG-1 (human myelomonocytic cell line) cells. The present sequence
 is human active IL-18 protein.

Sequence 157 AA;
 Query Match 99.9%; Score 811; DB 23; Length 157;
 Best Local Similarity 99.4%; Pred. No. 7.2e-83;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTFIISMYKDSQPRGM 60
|||||
DB 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTFIISMYKDSQPRGM 60
|||||
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
|||||
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
|||||
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
|||||
DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
|||||
RESULT 8
AAEI7134
ID AAEI7134 standard; Protein; 157 AA.
XX
AC AAEI7134;
XX
DT 22-APR-2002 (first entry)
XX
DE Human IL-18 protein.
XX
KW Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV;
KW influenza virus; human immunodeficiency virus; HIV; herpes simplex virus;
KW hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus;
KW HPV; hepatitis C virus; HCV.
XX
OS Homo sapiens.
XX
PN WO200193898-A1.
XX
PD 13-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US17924.
XX
PR 02-JUN-2000; 2000US-208869P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Esser KM, Rosenberg M, Tal-Singer R, Woodnutt G, Chisari FV;
XX
DR WPI; 2002-154554/20.
XX
PT Treatment of disease caused by e.g. influenza virus comprises
PT administration of composition containing polypeptide, having identity
PT of amino acid sequences -
XX
PS Claim 1; Fig 1; 4lpp; English.
XX
CC The invention relates to a method for treating viral diseases with
CC IL-18, also known as interferon-gamma-inducing factor (IGIF) and IL-18
CC combinations. The method involves administering a composition
CC comprising IL-18 and IL-18 in combination with other agents. The method
CC is used for treating diseases caused by viruses such as influenza virus,
CC human immunodeficiency virus (HIV), herpes simplex virus (HSV),
CC hepatitis A virus (HAV), hepatitis B virus (HBV), human papillomavirus
CC (HPV) and hepatitis C virus (HCV). The present sequence is human
CC IL-18 protein.
XX
SQ Sequence 157 AA;
Query Match 99.9%; Score 811; DB 23; Length 157;
Best Local Similarity 99.4%; Pred. No. 7.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTFIISMYKDSQPRGM 60
|||||
DB 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTFIISMYKDSQPRGM 60
|||||
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
|||||

DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
|||||
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
|||||
DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
|||||
RESULT 9
AAAY85167
ID AAY85167 standard; Protein; 158 AA.
XX
AC AAY85167;
XX
DT 23-JUN-2000 (first entry)
XX
DE Human interleukin-18 (IL-18) amino acid sequence.
XX
KW Interleukin-18; production; IL-18; human; medical injection product.
XX
OS Homo sapiens.
XX
PN CN1243130-A.
XX
PD 02-FEB-2000.
XX
PF 24-JUL-1998; 98CN-0103307.
XX
PR 24-JUL-1998; 98CN-0103307.
XX
PA (WUGG/) WU G.
XX
PI Wu G, Liu Z;
XX
DR WPI; 2000-340020/30.
XX
DR N-PSDB; AAA10526.
XX
PT Preparation method for engineering bacteria for recombination of human
PT interleukin-18 and its product thereof -
XX
PS Claim 1; Page 2; 17pp; English.
XX
CC This sequence represents the human interleukin-18 (IL-18) amino acid
CC sequence. The invention relates to a method for engineering bacterium for
CC recombination of human IL-18 and a method for the preparation of IL-18. A
CC primer containing a restriction endonuclease site can be used to
CC accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
CC stop codon preferred by coli bacillus to raise the expression rate. The
CC method uses a high-amplification culture medium to increase the
CC expression level and only requires a one-step purification process to
CC obtain a medical injection-pure product.
XX
SQ Sequence 158 AA;
Query Match 99.9%; Score 811; DB 21; Length 158;
Best Local Similarity 99.4%; Pred. No. 7.2e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTFIISMYKDSQPRGM 60
|||||
DB 2 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDNRNAPRTFIISMYKDSQPRGM 61
|||||
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
|||||
DB 62 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 121
|||||
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
|||||
DB 122 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 158
|||||
RESULT 10
AAW48959
ID AAW48959 standard; Peptide; 180 AA.
|||||

XX AAW48959;
AC
XX
DT
XX
DE Wild-type human interferon-gamma inducing factor.
XX
KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "Signal peptide"
FT Protein 24..180
FT /note= "Mature human IGIF which is claimed by the
FT inventors under claim 3 in the specification"
XX
XX EP845530-A2.
XX
XX
PD 03-JUN-1998.
XX
XX 28-NOV-1997; 97EP-0309632.
XX
XX 14-NOV-1997; 97JP-0329715.
XX 29-NOV-1996; 96JP-0333037.
XX 21-JAN-1997; 97JP-0020906.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX KurImoto M, Okamoto I, Yamamoto K;
XX
XX WPI; 1998-288747/26.
XX N-PSDB; AAV32754.
XX
XX Mutants of interferon-gamma inducing polypeptide - useful as
XX antitumour, antiviral, antimicrobial or anti-immunopathic agents
XX
XX Claim 3; pages 36-37; 59pp; English.
XX
XX The present sequence represents the wild-type human interferon-gamma
XX inducing factor (IGIF). The invention provides for mutant human and
XX mouse interferon-gamma inducing factors in which one or more cysteine
XX residues are replaced with different residues at or away from the
XX consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
XX capable of stimulating immunocompetent cells for the production of
XX interferon-gamma and are claimed to be less toxic, more active and
XX stable than the corresponding wild type IGIF. The mutant IGIFs are also
XX claimed to enhance killer cell cytotoxicity and/or induce killer cell
XX formation, and may therefore be useful as antitumour agents, antitumour
XX immunotherapeutics, antiviral agents and antimicrobial agents. The
XX mutant IGIFs are also claimed to be useful for treating hepatitis,
XX acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
XX malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
XX thrombopenia caused by radiation- and chemo-therapy.
XX
XX Sequence 180 AA;

Query Match 99.9%; Score 811; DB 19; Length 180;
Best Local Similarity 99.4%; Pred. No. 8.6e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 60
DB 24 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 83
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNINKDTSIIFFORSVPGHDKNQFESSY 120
DB 84 AVTISVKCEKISLSCENKIISFKEMNPPDNINKDTSIIFFORSVPGHDKNQFESSY 143

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 144 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 180

RESULT 11
AAW22047

ID AAW22047 standard; Protein; 193 AA.

AC AAW22047;

DT 14-JAN-1998 (first entry)

XX Interferon gamma inducing factor-2 (IGIF-2) protein.

DE Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte;
KW inflammation; proliferation; differentiation; maturation; tissue damage;
KW human.

OS Homo sapiens.

XX WO9724441-A1.

XX 10-JUL-1997.

XX 20-DEC-1996; 96WO-US20432.

XX 29-DEC-1995; 95US-0580667.

XX (INCY-) INCYTE PHARM INC.

XX Cocks BG, Coleman R, Hawkins PR;

XX WPI; 1997-363677/33.

XX N-PSDB; AAV74987.

XX Novel interferon gamma inducing factor-2 - used to screen for
XX compounds to diagnose, treat or prevent tissue damage associated
XX with inflammation

XX Claim 1; Page 46; 60pp; English.

XX This is the protein sequence of interferon gamma inducing factor-2
XX (IGIF-2). An IGIF-2 variant (AAW31757) and an IGIF variant (AAW22049),
XX which may be an alternate transcript, also exist. Probes derived from
XX the nucleic acid sequences can be used to quantify the expression of
XX IGIF-2 in conditions that are associated with inflammation or aberrant
XX expression of IGIF-2. The protein can be used to screen for compounds
XX that interact with IGIF-2, such as antibodies, antagonists or other
XX inhibitors (especially ribozymes or antisense sequences) of IGIF-2
XX expression or activity. The protein can also be used to diagnose,
XX prevent or treat IGIF-2 induction of proliferation, differentiation or
XX maturation of leucocytes or lymphocytes, especially in relation to tissue
XX damage associated with inflammation.

XX Sequence 193 AA;

Query Match 99.9%; Score 811; DB 18; Length 193;
Best Local Similarity 99.4%; Pred. No. 9.5e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 60

DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 96

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNINKDTSIIFFORSVPGHDKNQFESSY 120

DB 97 AVTISVKCEKISLSCENKIISFKEMNPPDNINKDTSIIFFORSVPGHDKNQFESSY 156

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 12
AAW46592
ID AAW46592 standard; Protein; 193 AA.
XX
XX AAW46592;
XX
XX 21-MAY-1998 (first entry)
DT
DE Amino acid sequence of human interleukin-1-gamma.
XX
XX Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;
KW induction; antibody; diagnostic assay; fusion protein; activity;
KW immunological disorder; allergy.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Region 41..47
FT /note= "beta-1 region"
FT Region 55..59
FT /note= "beta-2 region"
FT Region 64..68
FT /note= "beta-3 region"
FT Region 83..88
FT /note= "beta-4 region"
FT Region 96..102
FT /note= "beta-5 region"
FT Region 108..113
FT /note= "beta-6 region"
FT Region 115..120
FT /note= "beta-7 region"
FT Region 137..143
FT /note= "beta-8 region"
FT Region 147..153
FT /note= "beta-9 region"
FT Region 160..164
FT /note= "beta-10 region"
FT Region 170..175
FT /note= "beta-11 region"
FT Region 187..191
FT /note= "beta-12 region"
XX
XX WO9744468-A1.
XX
XX 27-NOV-1997.
XX
XX 16-MAY-1997; 97WO-US07282.
XX
XX 20-MAY-1996; 96US-0651998.
XX
XX (SCHE) SCHERING CORP.
XX
XX Bazan JF, Hardman GT, Kastelein RA, Sana TR, Timans JC;
PI
XX
XX WPI; 1998-018522/02.
DR N-PSDB; AAW05368.
XX
XX Antagonist of human interleukin-1-gamma - used for treating
PT immunological disorders caused by human IL-1-gamma
XX
XX Disclosure; Pages 54-55; 63pp; English.
XX
XX The present sequence represents human interleukin-1-gamma (IL-1-gamma).
CC The protein is the human equivalent of a mouse cytokine, IGIF, which
CC induces certain T cells to produce interferon-gamma. Human IL-1-gamma
CC and mouse IGIF show 71% identity at the nucleotide level and
CC approximately 65% identity at the amino acid level. Antagonists of
CC IL-1 gamma, e.g. antibodies, can be used in a method for treating a
CC condition caused by human IL-1 gamma. The antibodies can also be used
CC in diagnostic assays. The IL-1-gamma protein can be covalently
CC conjugated to polyethylene glycol or to a polypeptide, and the fusion
CC protein used in a pharmaceutical composition for supplying the

CC biological activity of IL-1 gamma. Conditions that can be treated using
CC the human IL-1-gamma protein include immunological disorders, allergies,
CC and infectious diseases. The IL-1-gamma can also be used to detect the
CC presence of the protein or its receptor.
XX
SQ Sequence 193 AA;
Query Match 99.9%; Score 811; DB 19; Length 193;
Best Local Similarity 99.4%; Pred. No. 9.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKSLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFITISMYKDSQPRGM 60
DB 37 YFGKLESKSLVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFITISMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNITKTSIIIFQSVPGHDNKMQFESSY 120
DB 97 AVTISVKCEKISLSCENKIISFKEMNPPDNITKTSIIIFQSVPGHDNKMQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193
RESULT 13
AAB30541
ID AAB30541 standard; Protein; 193 AA.
XX
XX AAB30541;
XX
XX 06-MAR-2001 (first entry)
DT
DE A human IL-18 with a caspase-8 cleavage site.
XX
XX Protease cleavage site; caspase-1; Interleukin-18; IL-18; protease.
KW
XX
XX Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Cleavage-site 33..36 /note= "caspase-8 cleavage site"
FT
XX
XX WO200061768-A2.
XX
XX 19-OCT-2000.
XX
XX 13-APR-2000; 2000WO-IL00220.
PF
XX
XX 13-APR-1999; 99IL-0129427.
PR
XX
XX (YEDA) YEDA RES & DEV CO LTD.
PA
XX
XX Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;
PI
XX
XX WPI; 2001-006910/01.
DR N-PSDB; AAC62200.
XX
XX Preparation of biologically active molecules from its inactive
PT precursors, comprises mutating their native cleavage site to a site
PT capable of being cleaved by protease and cleaving the mutated molecule
PT
XX
XX Disclosure; Fig 8a-b; 40pp; English.
PS
XX The present sequence represents a human pro interleukin-18 (IL-18)
CC with a caspase-8 cleavage site. The natural cleavage site of IL-18
CC was mutated to a site susceptible to cleavage by a common protease.
CC The specification describes a method for the preparation of biologically
CC active molecules from their biologically inactive precursors. The method
CC comprises mutating the native cleavage site to a site capable of being
CC cleaved by a protease and cleaving the mutated molecule to yield the
CC active compound. The method is especially used to produce active

CC cytokines, such as IL-18.

XX Sequence 193 AA;

Query Match 99.9%; Score 811; DB 22; Length 193;
Best Local Similarity 99.4%; Pred. NO. 9.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSIIFFORSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSIIFFORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 14

AAG63830
ID AAG63830 standard; Protein; 193 AA.

XX AC AAG63830;

XX DT 26-NOV-2001 (first entry)
XX DE Amino acid sequence of human interleukin 18 (IL-18).

XX KW T-cell-helper type 2 response; Th2 response; T cell mediated response;
XX KW allergic response; interleukin 18; IL-18; IgE-mediated allergy;
XX KW allergic asthma; anaphylactic reaction; asthma associated allergy;
XX KW IgE dependent allergic rhinoconjunctivitis.

XX OS Homo sapiens.

XX PN WO200168896-A1.

XX PD 20-SEP-2001.

XX PF 02-MAR-2001; 2001WO-US06869.

XX PR 10-MAR-2000; 2000US-0188311.

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX PI Levy S, Dekruffy RH, Umetsu DT, Maecker H;

XX DR WPI; 2001-570874/64.

XX DR N-PSDB; AAH78060.

XX PT Reducing antigen specific immune response in conditions such as asthma,
XX PT allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
XX PT antigen-specific allergic response -
XX PS Disclosure; Page 36; 38pp; English.

XX CC The specification describes a method for reducing a T-cell-helper
XX CC type 2 (Th2) T cell mediated antigen-specific allergic response. The
XX CC method comprises administering a DNA construct encoding a fusion
XX CC protein of interleukin 18 (IL-18) and an antigen associated with the
XX CC allergic response. The method is useful for reducing a Th2 T cell
XX CC mediated antigen-specific allergic response especially IgE-mediated
XX CC allergic asthma or anaphylactic reactions or IgE dependent allergic
XX CC rhinoconjunctivitis, and for treating asthma associated allergies where
XX CC the allergies are ongoing at the time of the administration. The
XX CC present sequence represents a human IL-18, and is used to construct
XX CC fusion proteins of the invention.

XX Sequence 193 AA;

XX Query Match 99.9%; Score 811; DB 23; Length 193;

XX Best Local Similarity 99.4%; Pred. NO. 9.5e-83;

Query Match 99.9%; Score 811; DB 22; Length 193;
Best Local Similarity 99.4%; Pred. NO. 9.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSIIFFORSVPGHDKMKQFESSY 120
DB 97 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTSIIFFORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 15

AAE16953
ID AAE16953 standard; Protein; 193 AA.

XX AC AAE16953;

XX DT 18-APR-2002 (first entry)

XX DE Human precursor interleukin-18 (Pro-IL-18) protein.

XX KW Human; precursor interleukin-18; pro-IL-18; caspase; interferon gamma;
XX KW IFN-gamma; immunocompetent.
XX OS Homo sapiens.

XX PN WO200198455-A2.

XX PD 27-DEC-2001.

XX PF 11-JUN-2001; 2001WO-US18804.

XX PR 15-JUN-2000; 2000US-211832P.

XX PR 10-AUG-2000; 2000US-224128P.

XX PR 20-JAN-2001; 2001US-264923P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Kirkpatrick RB, Shatzman AR, Ho YS, Mcdevitt P;

XX DR WPI; 2002-139786/18.

XX DR N-PSDB; AAD27364.

XX PT Activation of precursor polypeptide e.g. interleukin-18 polypeptide
XX PT useful for inducing interferon-gamma production, comprises contacting
XX PT or co-expressing caspase 4 or caspase 5 with precursor polypeptide -
XX PS Claim 7; Fig 1; 64pp; English.

XX CC The invention relates to a method for the in vitro activation of human
XX CC precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
XX CC method comprises contacting precursor IL-18 with an activating enzyme
XX CC such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
XX CC of cysteine proteases that include interleukin-beta converting enzyme
XX CC (ICE), which preferentially cleave substrates containing a protease
XX CC activation motif. The methods are useful for producing physiologically
XX CC active polypeptide e.g. active IL-18 polypeptide. The active IL-18
XX CC polypeptide has an activity of inducing the production of interferon
XX CC (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
XX CC biologically active substance for stimulating the production of IFN-gamma
XX CC from KG-1 (human myelomonocytic cell line) cells. The present sequence
XX CC is human Pro-IL-18 protein.

XX Sequence 193 AA;

XX Query Match 99.9%; Score 811; DB 23; Length 193;

XX Best Local Similarity 99.4%; Pred. NO. 9.5e-83;


```
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLEFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLDQVLFIDQGNRPLEFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 96
Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 120
Db 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKMQFESSY 156
Qy 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 193
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OM protein - protein search, using sw model

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(without alignments)
329.957 Million cell updates/sec

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Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 810 | 99.8 | 157 | 2 | US-08-896-605A-6 |
| 2 | 810 | 99.8 | 157 | 2 | US-08-896-501A-4 |
| 3 | 810 | 99.8 | 157 | 3 | US-08-884-324-1 |
| 4 | 810 | 99.8 | 157 | 3 | US-08-996-338-26 |
| 5 | 810 | 99.8 | 157 | 4 | US-08-558-818-1 |
| 6 | 810 | 99.8 | 157 | 4 | US-08-974-469A-1 |
| 7 | 810 | 99.8 | 157 | 4 | US-08-832-180-1 |
| 8 | 810 | 99.8 | 157 | 4 | US-08-832-198-6 |
| 9 | 810 | 99.8 | 157 | 4 | US-09-819-902-6 |
| 10 | 810 | 99.8 | 157 | 4 | US-09-752-510-6 |
| 11 | 810 | 99.8 | 193 | 2 | US-08-896-605A-2 |
| 12 | 810 | 99.8 | 193 | 2 | US-08-896-501A-2 |
| 13 | 810 | 99.8 | 193 | 4 | US-08-832-180-9 |
| 14 | 792 | 97.5 | 193 | 4 | US-09-597-576-2 |
| 15 | 513 | 63.2 | 157 | 2 | US-08-502-535B-2 |
| 16 | 513 | 63.2 | 157 | 2 | US-08-908-005A-2 |
| 17 | 513 | 63.2 | 157 | 3 | US-08-996-338-27 |
| 18 | 513 | 63.2 | 157 | 4 | US-08-558-818-7 |
| 19 | 513 | 63.2 | 157 | 4 | US-08-974-469A-7 |
| 20 | 513 | 63.2 | 157 | 4 | US-08-832-180-8 |
| 21 | 513 | 63.2 | 157 | 4 | US-08-832-198-11 |
| 22 | 513 | 63.2 | 157 | 4 | US-09-253-523-2 |
| 23 | 513 | 63.2 | 157 | 4 | US-09-251-911-2 |
| 24 | 513 | 63.2 | 157 | 4 | US-09-819-902-11 |
| 25 | 513 | 63.2 | 157 | 4 | US-09-819-902-11 |
| 26 | 259 | 31.9 | 50 | 4 | US-08-832-198-2 |
| 27 | 259 | 31.9 | 50 | 4 | US-09-819-902-2 |

| | | | | | | |
|----|------|------|-----|---|---------------------|--------------------|
| 28 | 259 | 31.9 | 50 | 4 | US-09-752-510-2 | Sequence 2, Appl |
| 29 | 96 | 11.8 | 25 | 4 | US-08-558-818-4 | Sequence 4, Appl |
| 30 | 96 | 11.8 | 25 | 4 | US-08-974-469A-4 | Sequence 4, Appl |
| 31 | 96 | 11.8 | 25 | 4 | US-08-832-180-4 | Sequence 4, Appl |
| 32 | 96 | 11.8 | 25 | 4 | US-08-832-198-8 | Sequence 8, Appl |
| 33 | 96 | 11.8 | 25 | 4 | US-09-819-902-8 | Sequence 8, Appl |
| 34 | 96 | 11.8 | 25 | 4 | US-09-752-510-8 | Sequence 8, Appl |
| 35 | 90 | 11.1 | 17 | 4 | US-08-832-198-5 | Sequence 5, Appl |
| 36 | 90 | 11.1 | 17 | 4 | US-09-819-902-5 | Sequence 5, Appl |
| 37 | 81 | 10.0 | 155 | 6 | 5494663-8 | Sequence 5, Appl |
| 38 | 81 | 10.0 | 267 | 2 | 5494663-5 | Patent No. 5494663 |
| 39 | 76.5 | 9.4 | 270 | 6 | US-08-611-880-1 | Sequence 1, Appl |
| 40 | 76.5 | 9.4 | 270 | 4 | US-09-085-305-13 | Sequence 13, Appl |
| 41 | 75.5 | 9.3 | 270 | 4 | US-09-085-305-20 | Sequence 20, Appl |
| 42 | 75.5 | 9.2 | 267 | 4 | US-09-134-001C-3520 | Sequence 3520, Ap |
| 43 | 73 | 9.0 | 270 | 4 | US-09-085-305-14 | Sequence 14, Appl |
| 44 | 73 | 9.0 | 270 | 4 | US-09-085-305-18 | Sequence 18, Appl |
| 45 | 72.5 | 8.9 | 268 | 4 | US-09-085-305-18 | Sequence 18, Appl |

ALIGNMENTS

RESULT 1
US-08-896-605A-6
; Sequence 6, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-605A-6

Query Match 99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
|||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKCNKIISFKENPNPNIDKTSKDIIFQFORSVPGHDKNMKFESSY 120
|||||
Db 61 AVTISVKCEKISXLSKCNKIISFKENPNPNIDKTSKDIIFQFORSVPGHDKNMKFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
|||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
RESULT 2
US-08-896-501A-4
; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896, 501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-896-501A-4
Query Match 99.8%; Score 810; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
|||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKCNKIISFKENPNPNIDKTSKDIIFQFORSVPGHDKNMKFESSY 120
|||||
Db 61 AVTISVKCEKISXLSKCNKIISFKENPNPNIDKTSKDIIFQFORSVPGHDKNMKFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
|||||

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
RESULT 3
US-08-884-324-1
; Sequence 1, Application US/08884324
; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takatori OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masahi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884, 324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-884-324-1
Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
|||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKCNKIISFKENPNPNIDKTSKDIIFQFORSVPGHDKNMKFESSY 120
|||||
Db 61 AVTISVKCEKISXLSKCNKIISFKENPNPNIDKTSKDIIFQFORSVPGHDKNMKFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
|||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSINFTVQNE 157
RESULT 4
US-08-996-338-26
; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takatori
; APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ. ID. NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
Qy 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNMQFESSY 120
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
TITLE OF INVENTION: WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: JP 58,240/95
PRIOR APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ. ID. NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIIISMYKDSQPRGM 60
Qy 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNMQFESSY 120
Db 61 AVTISVCKEKISXLSKCNKIISFKEMNPPDNKDKSDIIFQFQSVPGHDKNMQFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENYUJO
APPLICANT: TORIGOE, Kakujl
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-1A
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
|||||
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCKISKXLSCKENKIISFKENPPDNKDKTSDIIFQORSVPGHDNKMQFESSY 120
|||||
DB 61 AVTISVKCKISKXLSCKENKIISFKENPPDNKDKTSDIIFQORSVPGHDNKMQFESSY 120
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
|||||
DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 7
US-08-832-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimpei
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-1

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
|||||
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCKISKXLSCKENKIISFKENPPDNKDKTSDIIFQORSVPGHDNKMQFESSY 120
|||||
DB 61 AVTISVKCKISKXLSCKENKIISFKENPPDNKDKTSDIIFQORSVPGHDNKMQFESSY 120
QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157
|||||
DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-08-832-198-6
Sequence 6, Application US/08832198
Patent No. 6242255
GENERAL INFORMATION:
APPLICANT: AKITA, Kenji
APPLICANT: NUKADA, Yoshiyuki
APPLICANT: FUJII, Mitsukiyo
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,198
FILING DATE: 08-APR-1997
CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/721,018
;; FILING DATE: 25-SEP-1996
;; APPLICATION NUMBER: JP 95-270725
;; FILING DATE: 26-SEP-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 96-067434
;; FILING DATE: 29-FEB-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP not yet received
;; FILING DATE: 20-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: AKITA-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-5197
;; TELEFAX: (202) 737-3528
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 157 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; OTHER INFORMATION: "Xaa" in position 73 is either
;; 'Ile' or 'Thr'
;; US-08-832-198-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMCFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMCFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-09-819-902-6
Sequence 6, Application US/09819902
Patent No. 6403079
GENERAL INFORMATION:
APPLICANT: AKITA, Kenji
NUKADA, Yoshiyuki
FUJII, Mitsukiyo
TANIMOTO, Tadao
KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
PRODUCTION BY IMMUNOCOMPETENT CELL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/819,902
;; FILING DATE: 29-Mar-2001
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/832,798
;; FILING DATE: 25-SEP-1996
;; APPLICATION NUMBER: JP 95-270725
;; FILING DATE: 26-SEP-1995
;; APPLICATION NUMBER: JP 96-067434
;; FILING DATE: 29-FEB-1996
;; APPLICATION NUMBER: JP not yet received
;; FILING DATE: 20-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: AKITA-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-5197
;; TELEFAX: (202) 737-3528
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 157 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; OTHER INFORMATION: "Xaa" in position 73 is either
;; 'Ile' or 'Thr'
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;; US-09-819-902-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMCFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSIIFFQRSVPGHDNKMCFESSY 120
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-09-752-510-6
Sequence 6, Application US/09752510
Patent No. 6441138
GENERAL INFORMATION:
APPLICANT: AKITA, Kenji
NUKADA, Yoshiyuki
FUJII, Mitsukiyo
TANIMOTO, Tadao
KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
PRODUCTION BY IMMUNOCOMPETENT CELL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,510
FILING DATE: 03-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,018
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 96-067434
FILING DATE: 29-FEB-1996
APPLICATION NUMBER: JP not yet received
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: AKITA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "xaa" in position 73 is either
'ile' or 'thr'
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-752-510-6

Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
Db 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKSDIIFQFORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKSDIIFQFORSVPGHDKMKQFESSY 120
QY 121 EGYFLACERKDLFLKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACERKDLFLKLLKKEDELGDRSIMFTVQNEED 157

RESULT 11
US-08-896-605A-2
Sequence 2, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 JULY 1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-2
Query Match 99.8%; Score 810; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKSDIIFQFORSVPGHDKMKQFESSY 120
Db 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKSDIIFQFORSVPGHDKMKQFESSY 156
QY 121 EGYFLACERKDLFLKLLKKEDELGDRSIMFTVQNEED 157
Db 157 EGYFLACERKDLFLKLLKKEDELGDRSIMFTVQNEED 193
RESULT 12
US-08-896-501A-2
Sequence 2, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 99.8%; Score 810; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 96
Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDKTSIIFFQRSVPVGHDKMKQFESSY 120
Db 97 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDKTSIIFFQRSVPVGHDKMKQFESSY 156
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 13

US-08-832-180-9
Sequence 9, Application US/08832180
Patent No. 6214584

GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakuiji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832.180
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 99.8%; Score 810; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 96
Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDKTSIIFFQRSVPVGHDKMKQFESSY 120
Db 97 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDKTSIIFFQRSVPVGHDKMKQFESSY 156
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 14

US-09-597-576-2
Sequence 2, Application US/09597576
Patent No. 6432678

GENERAL INFORMATION:
APPLICANT: Alexander Taylor
APPLICANT: Han Trinh
TITLE OF INVENTION: MACACA CYNOMOLGUS IL18
FILE REFERENCE: GP-70629
CURRENT APPLICATION NUMBER: US/09/597,576
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/140,140
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: MACACA CYNOMOLGUS
US-09-597-576-2

Query Match 97.5%; Score 792; DB 4; Length 193;
Best Local Similarity 95.5%; Pred. No. 5.7e-86;
Matches 150; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60
Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 96
Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDKTSIIFFQRSVPVGHDKMKQFESSY 120
Db 97 AVAISVKCEKISTLSCEKNKIIISFKEMNPPDNIKDKTSIIFFQRSVPVGHDKMKQFESSY 156
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 15

US-08-502-535B-2
Sequence 2, Application US/08502535B
Patent No. 5912324

GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakuiji
APPLICANT: KUNIKATA, Toshio

```

; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
; TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,535B
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184162/1994
; FILING DATE: 14-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 45057/1995
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKAMURA-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-502-535B-2

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Query Match      63.2%; Score 513; DB 2; Length 157;
Best Local Similarity 64.9%; Pred. NO. 4.3e-53;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;

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Db 2 FGRHCTTAVIRINDQVLEVDK-RQVFEDMTDIDQSAEPQTRLIYMYKDSQPRGMA 60

QY 62 VTISVKCEKISLSCENKIISFKEMNPPDNKDKTSDIFFQSVPGHDKMOPFESSYE 121
Db 61 VTLSVKDSKATLSCKNKIISFEMDPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119

QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
Db 120 GHFLACQKEDDAFKLILKKEDELGDRSIMFTVQN 153

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Search completed: April 4, 2003, 11:02:06
Job time: 15 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 11:01:31 ; Search time 34 seconds
(without alignments)
282.305 Million cell updates/sec

Title: US-09-716-356A-6
Perfect score: 812
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 811 | 99.9 | 157 | 9 | US-10-094-153-2 |
| 2 | 811 | 99.9 | 157 | 10 | US-09-775-046-9 |
| 3 | 811 | 99.9 | 157 | 12 | US-10-100-057-6 |
| 4 | 811 | 99.9 | 193 | 9 | US-09-770-528-8 |
| 5 | 811 | 99.9 | 193 | 10 | US-09-798-075-1 |
| 6 | 810 | 99.8 | 157 | 10 | US-09-924-099-21 |
| 7 | 807 | 99.4 | 157 | 9 | US-10-094-153-10 |
| 8 | 807 | 99.4 | 193 | 9 | US-10-094-153-9 |
| 9 | 805 | 99.1 | 157 | 9 | US-10-094-153-6 |
| 10 | 805 | 99.1 | 157 | 9 | US-10-094-153-7 |
| 11 | 805 | 99.1 | 193 | 9 | US-10-094-153-3 |
| 12 | 805 | 99.1 | 193 | 9 | US-10-094-153-4 |
| 13 | 801 | 98.6 | 157 | 12 | US-10-100-057-20 |
| 14 | 799 | 98.4 | 157 | 9 | US-10-094-153-8 |
| 15 | 799 | 98.4 | 193 | 9 | US-10-094-153-5 |
| 16 | 791 | 97.4 | 157 | 12 | US-10-100-057-21 |
| 17 | 791 | 97.4 | 157 | 12 | US-10-100-057-22 |
| 18 | 782 | 96.3 | 157 | 12 | US-10-100-057-25 |
| 19 | 781 | 96.2 | 157 | 12 | US-10-100-057-23 |

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|----|------|------|------|----|---------------------|-------------------|
| 20 | 772 | 95.1 | 157 | 12 | US-10-100-057-26 | Sequence 26, Appl |
| 21 | 771 | 95.0 | 157 | 12 | US-10-100-057-24 | Sequence 24, Appl |
| 22 | 634 | 78.1 | 157 | 10 | US-09-917-265-12 | Sequence 12, Appl |
| 23 | 634 | 78.1 | 192 | 10 | US-09-917-265-8 | Sequence 8, Appl |
| 24 | 610 | 75.1 | 154 | 10 | US-09-917-265-5 | Sequence 5, Appl |
| 25 | 517 | 63.7 | 157 | 12 | US-10-100-057-27 | Sequence 27, Appl |
| 26 | 515 | 63.4 | 157 | 10 | US-09-775-046-8 | Sequence 8, Appl |
| 27 | 515 | 63.4 | 157 | 12 | US-10-100-057-7 | Sequence 7, Appl |
| 28 | 515 | 63.4 | 192 | 9 | US-09-770-528-9 | Sequence 9, Appl |
| 29 | 505 | 62.2 | 157 | 10 | US-09-924-099-22 | Sequence 22, Appl |
| 30 | 359 | 44.2 | 133 | 10 | US-10-100-057-28 | Sequence 28, Appl |
| 31 | 90 | 11.1 | 17 | 12 | US-10-100-057-13 | Sequence 13, Appl |
| 32 | 81 | 10.0 | 265 | 10 | US-09-815-242-5859 | Sequence 5859, Ap |
| 33 | 81 | 10.0 | 265 | 10 | US-09-815-242-12894 | Sequence 12894, A |
| 34 | 79 | 9.7 | 452 | 10 | US-09-881-7528-268 | Sequence 268, App |
| 35 | 74 | 9.1 | 467 | 10 | US-09-374-579-2 | Sequence 2, Appl |
| 36 | 71.5 | 8.8 | 467 | 10 | US-09-374-579-4 | Sequence 4, Appl |
| 37 | 71.5 | 8.8 | 831 | 10 | US-09-864-761-48702 | Sequence 48702, A |
| 38 | 71 | 8.7 | 14 | 12 | US-10-100-057-12 | Sequence 12, Appl |
| 39 | 70 | 8.6 | 4590 | 9 | US-10-160-758-13 | Sequence 13, Appl |
| 40 | 70 | 8.6 | 4590 | 9 | US-10-160-758-14 | Sequence 14, Appl |
| 41 | 69.5 | 8.6 | 6304 | 9 | US-10-147-026-16 | Sequence 16, Appl |
| 42 | 69 | 8.5 | 98 | 9 | US-09-970-033-2 | Sequence 2, Appl |
| 43 | 68.5 | 8.4 | 331 | 10 | US-09-924-841-4 | Sequence 4, Appl |
| 44 | 68.5 | 8.4 | 521 | 9 | US-09-820-843A-93 | Sequence 93, Appl |
| 45 | | | | | | |

ALIGNMENTS

RESULT 1
US-10-094-153-2
; Sequence 2, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094.153
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-153-2

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|---------------------------------------|--------|--------------------------------------------------------------|----------|------------|----|--------|------|
| Query Match | 99.98; | Score | 811; | DB | 9; | Length | 157; |
| Best Local Similarity | 99.48; | Pred. No. | 1.6e-75; | | | | |
| Matches | 156; | Conservative | 0; | Mismatches | 1; | Indels | 0; |
| Gaps | 0; | | | | | | |
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| Db | 1 | YFGKLESKLSVIRNLNDQVLFDQGNRPFLFEDMTDSDCRDNAPRTIFITISWKDSQPRGM | 60 | | | | |
| Qy | 61 | AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY | 120 | | | | |
| Db | 61 | AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY | 120 | | | | |
| Qy | 121 | EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE | 157 | | | | |
| Db | 121 | EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE | 157 | | | | |
| RESULT 2 | | | | | | | |
| US-09-775-046-9 | | | | | | | |
| ; Sequence 9, Application US/09775046 | | | | | | | |
| ; Patent No. US20020102234A1 | | | | | | | |

GENERAL INFORMATION:
APPLICANT: Debets, Johannes Eduard Maria Antonius
APPLICANT: Timans, Jacqueline C.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01073K
CURRENT APPLICATION NUMBER: US/09/775,046
PRIOR FILING DATE: 2001-02-01
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent in version 3.1
SEQ ID NO 9
LENGTH: 157
TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-046-9

Query Match 99.9%; Score 811; DB 10; Length 157;
Best Local Similarity 99.4%; Pred. No. 1.6e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKIIISFKEMNPPDNKDTKSDIIFQORSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNKDTKSDIIFQORSVPGHNDKMQFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 3
US-10-100-057-6
Sequence 6, Application US/10100057
Patent No. US20020150553A1
GENERAL INFORMATION:
APPLICANT: GILLISPIE, Matthew Todd
HORMOOD, Nicole Joy
UDAGAWA, No. US20020150555A1uyuki
KURIMOTO, Masashi
TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/100,057
FILING DATE: 19-Mar-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/030,061
FILING DATE: 25-FEB-1998
APPLICATION NUMBER: JP 55,468/1997
FILING DATE: 25-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25 618
REFERENCE/DOCKET NUMBER: GILLISPIE-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-100-057-6

Query Match 99.9%; Score 811; DB 12; Length 157;
Best Local Similarity 99.4%; Pred. No. 1.6e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKIIISFKEMNPPDNKDTKSDIIFQORSVPGHNDKMQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNKDTKSDIIFQORSVPGHNDKMQFESSY 120

QY 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 4
US-09-770-528-8
Sequence 6, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kastelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-770-528-8

Query Match          99.9%; Score 811; DB 9; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.1e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 120
DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 156

QY 121 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNEQ 157
DB 157 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNEQ 193

RESULT 5
US-09-798-075-1
; Sequence 1, Application US/09798075
; Patent No. US20010044418A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Shoshana
; APPLICANT: Dektyuff, Rosemarie
; APPLICANT: Umetsu, Dale
; APPLICANT: Maechler, Holden
; TITLE OF INVENTION: Treatment of Allergies
; FILE REFERENCE: STAN-179
; CURRENT APPLICATION NUMBER: US/09/798,075
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/188,311
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-075-1

Query Match          99.9%; Score 811; DB 10; Length 193;
Best Local Similarity 99.4%; Pred. No. 2.1e-75;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 96

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 120
DB 97 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 156

QY 121 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNEQ 157
DB 157 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNEQ 193

RESULT 6
US-09-924-099-21
; Sequence 21, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
```

```
;
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 21
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (73)
; OTHER INFORMATION: "Xaa" means an amino acid of isoleucine or threonine.
US-09-924-099-21

Query Match          99.8%; Score 810; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.1e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 120

QY 121 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNEQ 157
DB 121 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNEQ 157

RESULT 7
US-10-094-153-10
; Sequence 10, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-10

Query Match          99.4%; Score 807; DB 9; Length 157;
Best Local Similarity 98.7%; Pred. No. 4.2e-75;
Matches 155; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 120
DB 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDKTSIIFFQRSVPGHDNKKMFESSY 120
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QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8

US-10-094-153-9
; Sequence 9, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-9

Query Match 99.4%; Score 807; DB 9; Length 193;
Best Local Similarity 98.7%; Pred. No. 5.4e-75;
Matches 155; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60
|||||
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 96
|||||
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNINKDTKSDIIFQSVPGHDKNKQFESSY 120
|||||
Db 97 AVTISVKCEKISTLSCENKIISFKEMNPPDNINKDTKSDIIFQSVPGHDKNKQFESSY 156
|||||
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|||||
Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 193

RESULT 9

US-10-094-153-6
; Sequence 6, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; CURRENT FILING DATE: 2002-03-08
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-6

Query Match 99.1%; Score 805; DB 9; Length 157;
Best Local Similarity 98.7%; Pred. No. 6.7e-75;
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60
|||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60
|||||
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNINKDTKSDIIFQSVPGHDKNKQFESSY 120
|||||
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNINKDTKSDIIFQSVPGHDKNKQFESSY 120
|||||
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10

US-10-094-153-7
; Sequence 7, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-7

Query Match 99.1%; Score 805; DB 9; Length 157;
Best Local Similarity 98.7%; Pred. No. 6.7e-75;
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60
|||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRNAPRTIFIISMVKDSQPRGM 60
|||||
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNINKDTKSDIIFQSVPGHDKNKQFESSY 120
|||||
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNINKDTKSDIIFQSVPGHDKNKQFESSY 120
|||||
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
|||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11

US-10-094-153-3
; Sequence 3, Application US/10094153
; Patent No. US20020169291A1
; GENERAL INFORMATION:
; APPLICANT: Dinarello, Charles
; APPLICANT: Kim, Soo Hyun
; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
; FILE REFERENCE: 475
; CURRENT APPLICATION NUMBER: US/10/094,153
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,327
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-3

Query Match 99.1%; Score 805; DB 9; Length 193;
 Best Local Similarity 98.7%; Pred. No. 8.7e-75;
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 60
 Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 96
 Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQSVPGHDNKNMFESSY 120
 Db 97 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQSVPGHDNKNMFESSY 156
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 12

US-10-094-153-4
 Sequence 4, Application US/10094153
 Patent No. US20020169291A1
 GENERAL INFORMATION:
 APPLICANT: Dinarello, Charles
 APPLICANT: Kim, Soo Hyun
 TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
 FILE REFERENCE: 475
 CURRENT APPLICATION NUMBER: US/10/094,153
 CURRENT FILING DATE: 2002-03-08
 PRIOR APPLICATION NUMBER: 60/274,327
 PRIOR FILING DATE: 2001-03-08
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 4
 LENGTH: 193
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-4

Query Match 99.1%; Score 805; DB 9; Length 193;
 Best Local Similarity 98.7%; Pred. No. 8.7e-75;
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 60
 Db 37 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 96
 Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQSVPGHDNKNMFESSY 120
 Db 97 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQSVPGHDNKNMFESSY 156
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 Db 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 193

RESULT 13

US-10-100-057-20
 Sequence 20, Application US/10100057
 Patent No. US2002015055A1
 GENERAL INFORMATION:
 APPLICANT: GILLISPIE, Matthew Todd
 APPLICANT: HORWOOD, Nicole Joy
 APPLICANT: UDAGAWA, No. US2002015055A1
 APPLICANT: KURIMOTO, Masashi
 TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/100,057
 FILING DATE: 19-Mar-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/030,061
 FILING DATE: 25-FEB-1998
 APPLICATION NUMBER: JP 55,468/1997
 FILING DATE: 25-FEB-1997

NAME: BROWDY, Roger L.
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: GILLISPIE-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (402) 628-5197
 TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 157 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 US-10-100-057-20

Query Match 98.6%; Score 801; DB 12; Length 157;
 Best Local Similarity 98.7%; Pred. No. 1.7e-74;
 Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 60
 Db 1 YFGKLESLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMYKDSQPRGM 60
 Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQSVPGHDNKNMFESSY 120
 Db 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQSVPGHDNKNMFESSY 120
 Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 14

US-10-094-153-8
 Sequence 8, Application US/10094153
 Patent No. US20020169291A1
 GENERAL INFORMATION:
 APPLICANT: Dinarello, Charles
 APPLICANT: Kim, Soo Hyun
 TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
 FILE REFERENCE: 475
 CURRENT APPLICATION NUMBER: US/10/094,153
 CURRENT FILING DATE: 2002-03-08
 PRIOR APPLICATION NUMBER: 60/274,327
 PRIOR FILING DATE: 2001-03-08
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 157
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-8

Query Match 98.4%; Score 799; DB 9; Length 157;
Best Local Similarity 98.1%; Pred. No. 2.8e-74;
Matches 154; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISLSCENKIIISFKENPPDNKDKTSDIIFQORSVPGHDKMKQFESSY 120
Db 61 AVTISVKCEKISLSCENKIIISFKENPPDNKDKTSDIIFQORSVPGHDKMKQFESSY 120
QY 121 EGYFLACERERDLFKLILKKEDELGLDRSIMFTVQNE 157
Db 121 EGYFLACERERDLFKLILKKEDELGLDRSIMFTVQNE 157

RESULT 15
US-10-094-153-5
Sequence 5, Application US/10094153
Patent No. US20020169291A1
GENERAL INFORMATION:
APPLICANT: Rinareello, Charles
APPLICANT: Kim, Soo Hyun
TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
FILE REFERENCE: 475
CURRENT APPLICATION NUMBER: US/10/094,153
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,327
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 193
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-5

Query Match 98.4%; Score 799; DB 9; Length 193;
Best Local Similarity 98.1%; Pred. No. 3.5e-74;
Matches 154; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 96
QY 61 AVTISVKCEKISLSCENKIIISFKENPPDNKDKTSDIIFQORSVPGHDKMKQFESSY 120
Db 97 AVTISVKCEKISLSCENKIIISFKENPPDNKDKTSDIIFQORSVPGHDKMKQFESSY 156
QY 121 EGYFLACERERDLFKLILKKEDELGLDRSIMFTVQNE 157
Db 157 EGYFLACERERDLFKLILKKEDELGLDRSIMFTVQNE 193

Search completed: April 4, 2003, 11:09:43
Job time : 35 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:58:21 ; Search time 17 seconds
(without alignments)
887.830 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 515 | 63.4 | 192 | 2 S60226 | cytokine IGIF - mo |
| 2 | 85 | 10.5 | 381 | 2 T40341 | hypothetical prote |
| 3 | 82 | 10.1 | 263 | 2 T39487 | hypothetical prote |
| 4 | 81.5 | 10.0 | 270 | 1 S10532 | interleukin-1 alph |
| 5 | 80.5 | 9.9 | 866 | 2 C71509 | probable DNA polym |
| 6 | 79 | 9.7 | 452 | 2 D64583 | hypothetical prote |
| 7 | 78.5 | 9.7 | 204 | 2 T44357 | hypothetical prote |
| 8 | 78 | 9.6 | 473 | 2 T32038 | hypothetical prote |
| 9 | 77.5 | 9.5 | 1251 | 2 A56677 | neuronal cell cycl |
| 10 | 77 | 9.5 | 364 | 2 A81261 | probable periplasm |
| 11 | 76 | 9.4 | 632 | 2 T00679 | hypothetical prote |
| 12 | 76 | 9.4 | 747 | 2 E84698 | hypothetical prote |
| 13 | 75.5 | 9.3 | 192 | 2 S15661 | (2'-5')oligo(A) sy |
| 14 | 75.5 | 9.3 | 270 | 2 I46620 | interleukin-1 alph |
| 15 | 75.5 | 9.3 | 1036 | 2 H64245 | hypothetical prote |
| 16 | 75.5 | 9.3 | 1663 | 1 C3MS | complement C3 prec |
| 17 | 75 | 9.2 | 1064 | 1 S37450 | protein-tyrosine k |
| 18 | 75 | 9.2 | 2470 | 2 I50726 | cation-independent |
| 19 | 74.5 | 9.2 | 334 | 2 T04198 | hypothetical prote |
| 20 | 74.5 | 9.2 | 389 | 2 B69277 | TRK potassium upta |
| 21 | 74.5 | 9.2 | 467 | 2 A48713 | serine/threonine s |
| 22 | 74.5 | 9.2 | 1228 | 2 A57384 | multimerin, endoth |
| 23 | 74.5 | 9.2 | 1510 | 2 T16927 | hypothetical prote |
| 24 | 74 | 9.1 | 245 | 2 B90488 | hypothetical prote |
| 25 | 74 | 9.1 | 361 | 2 E96904 | minD family ATPase |
| 26 | 74 | 9.1 | 376 | 2 T24925 | hypothetical prote |
| 27 | 74 | 9.1 | 467 | 2 I49609 | proto-oncogene pro |
| 28 | 74 | 9.1 | 467 | 2 A47388 | serine/threonine p |
| 29 | 74 | 9.1 | 680 | 2 A28121 | major merozoite su |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 74 | 9.1 | 810 | 2 B71639 | virb4 protein prec |
| 31 | 74 | 9.1 | 1772 | 2 A45532 | major merozoite su |
| 32 | 73.5 | 9.1 | 268 | 2 H85641 | probable small sub |
| 33 | 73.5 | 9.1 | 268 | 2 C90781 | probable small sub |
| 34 | 73 | 9.0 | 418 | 2 D82932 | seryl-tRNA synthet |
| 35 | 73 | 9.0 | 447 | 2 T26293 | hypothetical prote |
| 36 | 72.5 | 8.9 | 268 | 1 B24073 | interleukin-1 alph |
| 37 | 72.5 | 8.9 | 313 | 2 C96528 | protein F27J15.10 |
| 38 | 72.5 | 8.9 | 436 | 2 G97701 | polynucleotide ade |
| 39 | 72.5 | 8.9 | 475 | 2 T32036 | hypothetical prote |
| 40 | 72.5 | 8.9 | 888 | 2 A38539 | p101 protein precu |
| 41 | 72.5 | 8.9 | 1246 | 2 S60954 | probable membrane |
| 42 | 72.5 | 8.9 | 1294 | 2 T48349 | EN2 protein - Ara |
| 43 | 72.5 | 8.9 | 1997 | 2 F71607 | DNA helicase II BR |
| 44 | 72 | 8.9 | 264 | 2 B90051 | hypothetical prote |
| 45 | 72 | 8.9 | 1613 | 2 S39059 | protein BRG1 - hum |

ALIGNMENTS

RESULT 1

S60226

Cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009; PMID:7477296

A:Accession: S60226

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OKA>

A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.4%; Score 515; DB 2; Length 192;

Best Local Similarity 64.9%; Pred. No. 2.7e-42;

Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

Qy 2 FQKLESKLSVIRNLNDQVLFDQGNRPLFEDMTDSDCRDNAPRTIFIISYKDSQPRGMA 61

Db 37 FGRLLHCTTAVIRNINDQVLFVDK-RQPVFEDMTDIDQSASEPQTRLIIIVMYKDSVIRGLA 95

Qy 62 VTISVCKEIKSLSCENKIIISFKEMNPPDNKDTKSDIIFQORSVPGHNDKNQFESSSYE 121

Db 96 VTLVSVDKSMSTLSCNKIIISFEENDPPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154

Qy 122 GFVLAACEERDLFKLLKKEDELGDRSIMFTVQN 155

Db 155 GHFLACQKEDDAFKLLKKEDENGDKSVMTLTN 188

RESULT 2

T40341

hypothetical protein SPBC3B9.02c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40341

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1997

A:Reference number: T21922

A:Accession: T40341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-381 <WOO>

A:Cross-references: EMBL:AL022070; PIDN:CAAI7782.1; GSPDB:GN00067; SPDB:SPBC3B9.02c

A:Experimental source: strain 972h-; cosmid c3B9

C:Genetics:

A:Gene: SPDB:SPBC3B9.02c

A:Map position: 2

```
Query Match          10.5%; Score 85; DB 2; Length 381;
Best Local Similarity 26.4%; Pred. No. 1.6;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;

QY 3 GKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFIISMVKDSQPRGMAY 62
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 208 GOLSSKDAF--DVNQRPTFLGMAKPVDSLTLDIWKPKTMF-----250

QY 63 TISVK-CEKISXLSKSCN-KIISF-KEMNPPDNKIDTKSDIIFQORSVPGHDKMKQFESSY 120
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 251 -LPVKPLESNALNSONEHTEVOKKSNIDNL--TPSELFRKRS---RDNNLSRSS---302

QY 121 EGYFLACEKERDLFLKLTKKKEDELGDRS 148
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 303 -----VSSKHLDYNSRNYNRDRDPDPT 325

RESULT 3
39487
hypothetical protein SPBC15D4.11c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T39487
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
A:Reference number: 221858
A:Accession: T39487
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-263 <LYN>
A:Cross-references: EMBL:AL031349; PIDN:CAA20486.2; GSPDB:GNO0067; SPDB:SPBC15D4.11c
A:Experimental source: strain 972h-; cosmid c15D4
C:Genetics:
A:Gene: SPDB:SPBC15D4.11c
A:Map position: 2
A:Introns: 96/2; 147/3
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match          10.1%; Score 82; DB 2; Length 263;
Best Local Similarity 21.7%; Pred. No. 2;
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTIFIISMVKDSQPRGMAYT 63
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 47 KLDSELYGVKQVLDLTPKKGYEKALHSFIHED-----PSLNYISALKEAKERIRVT 100

QY 64 ISVKCEKISXLSKSCN-KIISF-KEMNPPDNKIDTKSDIIFQORSVPGH-----109
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 101 VPVYSRKSXY--QTKPITHSAEN--ENGNETSDELVFFQHSIPAYVQLTNNHGTILCAL 156

QY 110 ---DNKMQFESSYEGYFLACEKERDLFLKLTKKKEDELGDR 147
   :||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 157 ILCKGMLHFDSDISFQSPQNSQAFSSDL-RLILQKSQYTKGR 196

RESULT 4
S10532
interleukin-1 alpha precursor - pig
N:Alternate names: hematopoietin-1; IL-1 alpha
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-Feb-1995 #sequence_revision 22-Nov-1996 #text_change 28-Jan-2000
C:Accession: S10532
R:Walliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.
Nucleic Acids Res. 18, 4282, 1990
A:Title: Porcine IL-1 alpha cDNA nucleotide sequence.
A:Reference number: S10532; MUID:90332454; PMID:2377484
A:Accession: S10532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <NAL>
A:Cross-references: EMBL:X52731; NID:g1987; PIDN:CAA36945.1; PID:g1988
```

```
C:Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte p
lls.
C:Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1alpha, unlike interleukin-1beta, is fully active.
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop
F;112/Domain: propeptide #status predicted <PRO>
F;113-270/Product: interleukin-1 alpha #status predicted <IL1>
F;82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match          10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 2.3;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

QY 8 KLSVIRNLNDQVLFIDQGNRPFLFEDMTD----SDCRDNAPRTI-FIISMVKDSQPRGMAY 62
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 123 KYNFMRVINHQCILNDARNOSIIRDPGGVYLMAAVLNLDVAKFDMAAVTSNDDSQLPV 182

QY 63 TISVKCEKISXLSKSCN-KIISF-KEM-NPPDNKIDTKSDIIFQORSVPGHDKMKQFESS 119
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 183 TLRIS-ETRLFVSAQNEDEPVLKELPETPTIKIDETSLFFWEK----HGNDYFKSAA 237

QY 120 YEGYFLACEKER 131
   :||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 238 HPKLFATATROEK 249

RESULT 5
C71509
probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: C71509
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A:Reference number: A71590; MUID:9900809; PMID:9784136
A:Accession: C71509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-866 <ARN>
A:Cross-references: GB:AE001322; GB:AE001273; NID:g328916; PIDN:AAC68093.1; PID:g332
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: pola
C:Superfamily: DNA-directed DNA polymerase I

Query Match          9.9%; Score 80.5; DB 2; Length 866;
Best Local Similarity 26.4%; Pred. No. 11;
Matches 34; Conservative 22; Mismatches 28; Indels 45; Gaps 8;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTD-----SDCRDNAPRTIFI 49
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 441 YFGMLASKLLAIKN----YLFVKLEEKGLKIDIFETVEQPLEAVLFAMEC-----V 486

QY 50 SMYKDSQPRGMAY---TISVKCEKIS-----XLSCKENKIISFKEMN-----PPDN 91
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 487 GMPLDQ--GLAVLDRLDLTKLEECQSEIYDLVGCCEFNKSPKQLSDILYQRLGIEPVDK 544

QY 92 IKDTKSDII 100
   ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 545 AKSTKAEVL 553

RESULT 6
D64583
hypothetical protein HP0508 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: D64583
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
```

K. FAIKHUTDINOV, V. V. WIESE, D. H. M. MUNGATTA, A. A. KETCEV, J. H. M. CHOUTENET, C. J. BOSSCHAM, D. J. CHITAMBA

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hy
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: AB1261
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73631.1; PID:g696906
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: CJ1643

Query Match 9.5%; Score 77; DB 2; Length 364;
Best Local Similarity 24.8%; Pred. No. 8.9;
Matches 38; Conservative 21; Mismatches 40; Indels 54; Gaps 9;

QY 12 IRNLNDQVLFIDQGNRPLFEDMTSDCRD-NAPRTFIISMVK- ----DSQPR----- 58
Db 211 LRKLNKILFADRGSTLYFQVLRDN--MDLNISTEFAKDLKSNFLPDSKPKPKITNFTS 268
QY 59 --GMATVISVKCEKI-----SXLSCEKNI-SFKEMNPPDNI----- 92
Db 269 NLGUTVNASLVTKIDPKSVSNAGFMVGDKILRVNNILNFKEL---QNILSAGNDFS 325
QY 93 -----KDTKSDIIFFQRSVPGH-----DNKMQF 115
Db 326 ILIERKSTKLPLSNFNELOGNANSGGDGKGFQF 358

RESULT 11
T00679
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F6E13.12
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00679; AB4873
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A:Reference number: Z14180
A:Accession: T00679
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-632 <ROU>
A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856
A:Experimental source: Cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10611797
A:Accession: AB4873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-632 <STO>
A:Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g43990; F6E13.12
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 632;
Best Local Similarity 25.6%; Pred. No. 21;
Matches 34; Conservative 29; Mismatches 40; Indels 30; Gaps 9;

QY 28 PLFEDMTSD-CRDNAPRTFIISMVKDSQPRGMATVISVKCBK-----ISXLSCEK 79
Db 368 PLSDRSASSDLCSNIGRSLSPMDIYKETRR---ISSLSPLNELFRFRFIHLSSCDGE 424
QY 80 IISFKF-----EMPNPNKIDTKDIIFFQRSVP--GHDNMQF--ESSSYEGVF-LACEK 129
Db 425 ASAFDTSPTCELPSEHLKDGKSSPL-----SVDTLGSENVIQTPESNSPDNYFGLSCSQ 480

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hy
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: AB1261
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73631.1; PID:g696906
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: CJ1643

Query Match 9.5%; Score 77; DB 2; Length 364;
Best Local Similarity 24.8%; Pred. No. 8.9;
Matches 38; Conservative 21; Mismatches 40; Indels 54; Gaps 9;

QY 12 IRNLNDQVLFIDQGNRPLFEDMTSDCRD-NAPRTFIISMVK- ----DSQPR----- 58
Db 211 LRKLNKILFADRGSTLYFQVLRDN--MDLNISTEFAKDLKSNFLPDSKPKPKITNFTS 268
QY 59 --GMATVISVKCEKI-----SXLSCEKNI-SFKEMNPPDNI----- 92
Db 269 NLGUTVNASLVTKIDPKSVSNAGFMVGDKILRVNNILNFKEL---QNILSAGNDFS 325
QY 93 -----KDTKSDIIFFQRSVPGH-----DNKMQF 115
Db 326 ILIERKSTKLPLSNFNELOGNANSGGDGKGFQF 358

RESULT 11
T00679
hypothetical protein At2g43990 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F6E13.12
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00679; AB4873
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A:Reference number: Z14180
A:Accession: T00679
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-632 <ROU>
A:Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212856
A:Experimental source: Cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10611797
A:Accession: AB4873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-632 <STO>
A:Cross-references: GB:AE002093; NID:g3212856; PIDN:AAC23407.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g43990; F6E13.12
A:Map position: 2

Query Match 9.4%; Score 76; DB 2; Length 747;
Best Local Similarity 24.7%; Pred. No. 26;
Matches 36; Conservative 29; Mismatches 59; Indels 22; Gaps 7;

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKDSQPRGMATV 63
Db 102 KLAHQQSVRRNARKV-----EEVGKQWDSQASEDERGKVILTLTYGEVLPE----T 150
QY 64 ISVCKBKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFFQ--SVPGHDNMQF-----SS 118
Db 151 ITPDMEKFK----RERTLLVAEENVFDSVLNHRDLVELERLISVDG--DDESEVECSSSS 205
QY 119 SYEGYFLACKEKDLFKLIILK-KEDE 143
Db 206 SSEGEKEEERREDVSKVVAVWTEDD 231

RESULT 13
S15661
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999
C:Accession: S15661; S19108
R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.
Nucleic Acids Res. 19, 1917-1924, 1991
A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked
A:Reference number: S15660; MUID:91232962; PMID:1709495
A:Accession: S15661
A:Molecule type: mRNA
A:Residues: 1-192 <RUT>
A:Cross-references: EMBL:X55982
R:Williams, B.
submitted to the EMBL Data Library, September 1990
A:Reference number: S19108
A:Accession: S19108
A:Molecule type: mRNA
A:Residues: 1-175, 'L', 177-192 <WIL>
A:Cross-references: EMBL:X55982; NID:g49714; PIDN:CAA39455.1; PID:g49715
C:Superfamily: oligo(A) synthetase
C:Keywords: nucleotidyltransferase

Query Match 9.3%; Score 75.5; DB 2; Length 192;
Best Local Similarity 23.2%; Pred. No. 5.8;
Matches 42; Conservative 24; Mismatches 50; Indels 65; Gaps 9;

QY 3 GKLESKLSVIRN-----LNDQVLFIDQGNRPLFEDMTSDCRDNAPRTFIISMVKD 54

Db 11 GRSDADLVVFLNLTSTFEDQLNQGVLIKEIKKQLCEVQHERRC----- 54
 QY 55 SPPRGMAVTISVKCEKISXLSCEKNIISPKENPNPNINIKDTKSDII----- 100
 Db 55 -----GVKFEVHSURSPNSRALSFK-LSAPDLKEVRFDPVPAYDLDHLNLIK 103
 QY 101 -----FFOR---SVP-CHDNKMFESSYEGYFLACE--KERDLFKLI-----LKKEDELG 145
 Db 104 PNOQFYANLISGVPAGKEGKLSICFWGLQKFLNCRPKLRLRLVTHWYQLCKE-KLG 162
 QY 146 D 146
 Db 163 D 163

RESULT 14
 I46620
 Interleukin-1 alpha precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 04-Feb-2000
 C:Accession: I46620
 R:Maliszewski, C.
 Nucleic Acids Res. 14, 4282, 1990
 A:Title: Nucleotide sequence of porcine Interleukin-1 alpha.
 A:Reference number: I46620
 A:Accession: I46620
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-270 <MAL>
 A:Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623
 C:Superfamily: Interleukin-1
 C:Keywords: lipoprotein; myristylation
 F:1-112/Domain: propeptide #status predicted <PRO>
 F:113-270/Product: interleukin-1 alpha #status predicted <IL1>
 F:82,83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 9.3%; Score 75.5; DB 2; Length 270;
 Best Local Similarity 22.0%; Pred. NO. 8.7;
 Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;
 QY 8 KLSYTRNLNDVLFIDOGNRPFLFEDWTD----SDCRDNAPRTI-FIISMYKDSQPRGMAY 62
 Db 123 KYNFMKVINHQICILNDARNQSIROPSGOYLMAVLNLDKAVKFDMAAYTSNDDSQLPV 182
 QY 63 TISVCKEIKISXLSCEK--KIISFKEM-NPPDNIKDKTSDIIFFQSRVPGHDKNMQFESS 119
 Db 183 TLRIS-ETRLVSAQNEDEPVLKELPETPKTIKDETSLLFFWEK----HGNMDYFKSAA 237
 QY 120 YEGYFLACEKER 131
 Db 238 HPKLLIATROEK 249

RESULT 15
 H64245
 Hypothetical protein MG414 - Mycoplasma genitalium
 C:Species: Mycoplasma genitalium
 C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 02-Mar-2001
 C:Accession: H64245; G64245
 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
 , C.A.; Venter, J.C.
 Science 270, 397-403, 1995
 A:Title: The minimal gene complement of Mycoplasma genitalium.
 A:Reference number: A64200; MUID:96026346; PMID:7569993
 A:Accession: H64245
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1036 <TIGR>
 A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046129; TIGR:MG414
 A:Experimental source: strain G-37
 A:Accession: G64245

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 'M', 310-1036 <TIG2>
 A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046128; TIGR:MG413
 A:Experimental source: strain G-37
 C:Genetics:
 A:Genetic code: SGC3
 A:Start codon: GTG
 C:Superfamily: hypothetical protein MG413
 Query Match 9.3%; Score 75.5; DB 2; Length 1036;
 Best Local Similarity 21.9%; Pred. NO. 43;
 Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;
 QY 14 NLNDQVLFIDOGNRPFLFED--MTDSDCRDNAPRTIFIISMYKDSQPRGMAYTISVKCEK- 70
 Db 845 SLNDEQLLVVDKLNITLSEKRLQTTKNVRFNKNKNKFNHLVENKQFNLFVDVDRSKKL 904
 QY 71 -ISXLSCEKNIISFKEMNPPDNIKDKTSDIIFFQSRVPGHDKNMQFESSYEGYFLACEK 129
 Db 905 FIKGVNDNQVFSISY-----DLKITNQTLIV-DANGFDNSINFDITS-----EN 950
 QY 130 ERDLFKLI---LKEDELGDRSIMEFTVQNE 157
 Db 951 QTQLFKALSFLKQNNLQFKRVDPDFNLKSQD 981
 Search completed: April 4, 2003, 11:01:47
 Job time : 20 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2003, 10:52:35 ; Search time 12 seconds
(without alignments)
542.649 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKREDELGDRSIMFTVQNEQ 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|------------|--------|--------------|
| 1 | 811 | 99.9 | 193 | 1 | IL18_HUMAN | Q14116 | homo sapien |
| 2 | 659 | 81.2 | 193 | 1 | IL18_HORSE | Q9xsq7 | equus caball |
| 3 | 654 | 80.5 | 193 | 1 | IL18_BOVIN | Q9tu73 | bos taurus |
| 4 | 637 | 78.4 | 192 | 1 | IL18_PIG | Q19073 | bos scrofa |
| 5 | 613 | 75.5 | 193 | 1 | IL18_CANFA | Q9xsro | canis famli |
| 6 | 515 | 63.4 | 192 | 1 | IL18_MOUSE | P70380 | mus musculu |
| 7 | 514.5 | 63.4 | 194 | 1 | IL18_RAT | P97636 | rattus norv |
| 8 | 81.5 | 10.0 | 270 | 1 | IL18_PIG | P18430 | bos scrofa |
| 9 | 81 | 10.0 | 267 | 1 | IL1A_RABIT | P04822 | oryctolagus |
| 10 | 77.5 | 9.5 | 674 | 1 | MUTL_CLOPE | Q8x186 | clostridium |
| 11 | 76.5 | 9.4 | 270 | 1 | IL1A_HORSE | Q28385 | equus caball |
| 12 | 75.5 | 9.3 | 192 | 1 | OASB_MOUSE | Q60856 | mus musculu |
| 13 | 75.5 | 9.3 | 1036 | 1 | Y414_MYCCE | P47653 | mycoplasma |
| 14 | 75.5 | 9.3 | 1663 | 1 | CO3_MOUSE | P01027 | mus musculu |
| 15 | 74.5 | 9.2 | 1228 | 1 | ECM_HUMAN | Q13201 | homo sapien |
| 16 | 74 | 9.1 | 467 | 1 | M3K8_MOUSE | Q07174 | mus musculu |
| 17 | 74 | 9.1 | 467 | 1 | M3K8_RAT | Q63562 | rattus norv |
| 18 | 74 | 9.1 | 1772 | 1 | MSP1_PLAYO | P13828 | plasmodium |
| 19 | 73 | 9.0 | 270 | 1 | IL1A_FELCA | O46613 | felis silve |
| 20 | 73 | 9.0 | 426 | 1 | YKXC_ASTLO | P98151 | astasia ion |
| 21 | 72.5 | 8.9 | 313 | 1 | COL4_ARATH | Q9m9b3 | arabidopsis |
| 22 | 71.5 | 8.8 | 268 | 1 | IL1A_BOVIN | P08831 | bos taurus |
| 23 | 71.5 | 8.8 | 467 | 1 | M3K8_HUMAN | P41279 | homo sapien |
| 24 | 71.5 | 8.8 | 527 | 1 | RAG2_HUMAN | P55895 | homo sapien |
| 25 | 71 | 8.7 | 700 | 1 | NONA_DROME | Q04047 | drosophila |
| 26 | 70.5 | 8.7 | 245 | 1 | KDSB_FUSNN | Q9rfa8 | fusobacteri |
| 27 | 70.5 | 8.7 | 268 | 1 | IL1A_CAPHI | P79161 | capra hircu |
| 28 | 70.5 | 8.7 | 644 | 1 | YGM4_YEAST | P53129 | saccharomyc |
| 29 | 70 | 8.6 | 198 | 1 | V511_ROTFA | P17467 | rabbit rota |
| 30 | 70 | 8.6 | 1647 | 1 | SN24_HUMAN | P15332 | homo sapien |
| 31 | 70 | 8.6 | 2663 | 1 | CENE_HUMAN | Q02224 | homo sapien |
| 32 | 70 | 8.6 | 4590 | 1 | FATH_HUMAN | Q14517 | homo sapien |
| 33 | 69.5 | 8.6 | 268 | 1 | IL1A_SHEEP | Q28579 | ovis aries |

RESULT 1

| ID | IL18_HUMAN | STANDARD; | PRT; | 193 AA. |
|----|----------------------------------------------------------------------------|-----------|------|---------|
| AC | Q14116; 075599; | | | |
| DT | 15-JUL-1998 (Rel. 36, Created) | | | |
| DT | 15-JUL-1998 (Rel. 36, Last sequence update) | | | |
| DE | Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor) | | | |
| DE | (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma). | | | |
| GN | IL18 OR IGIF. | | | |
| OS | Homo sapiens (Human) | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Liver; | | | |
| RX | MEDLINE=96247646; PubMed=8666798; | | | |
| RA | Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K., | | | |
| RA | Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T., | | | |
| RA | Fukuda S., Ikeda M., Okamura H., Kurimoto M.; | | | |
| RT | "Cloning of the cDNA for human IFN-gamma-inducing factor, expression | | | |
| RT | in Escherichia coli, and studies on the biologic activities of the | | | |
| RT | protein."; | | | |
| RL | J. Immunol. 156:4274-4279(1996). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Yong D., Guixin D., Lihua H., Haitao W.; | | | |
| RT | "Cloning and sequencing of the cDNA for precursor hIL-18."; | | | |
| RL | Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Liu J., Peng X., Yuan J., Qiang B.; | | | |
| RT | "Cloning of human Interleukin 18 cDNA."; | | | |
| RL | Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Urinary bladder; | | | |
| RA | Strausberg R.; | | | |
| RL | Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [5] | | | |
| RP | SEQUENCE OF 2-193 FROM N.A. | | | |
| RC | TISSUE=peripheral blood; | | | |
| RA | Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.; | | | |
| RL | Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases. | | | |
| CC | -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS | | | |
| CC | AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I | | | |
| CC | CELLS. | | | |
| CC | -1- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY. | | | |
| CC | ----- | | | |
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| CC | use by non-profit institutions as long as its content is in no way | | | |
| CC | modified and this statement is not removed. Usage by and for commercial | | | |

083090 treponema p
Q18610 caenorhabdi
P80093 capsicum an
P16716 capripoxvir
Q61739 mus musculu
Q9r0m0 mus musculu
Q9cp43 pasteurella
P24423 azotobacter
Q9vk89 drosophila
P01582 mus musculu
P08703 penicillium
P36166 saccharomyc

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CC CC
CC CC
CC CC
DR EMBL: D49950; BAA08706.1; -
DR EMBL: AF077611; AAC27787.1; -
DR EMBL: AY044641; AAK95950.1; -
DR EMBL: BC007007; AAH07007.1; -
DR EMBL: BC007461; AAH07461.1; -
DR EMBL: U90434; AAB50010.1; -
DR Genew: HGNC:5986; IL18.
DR MIM: 600953; -
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
KW Cytokine.
FT CHAIN 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CHAIN 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 81.2%; Score 659; DB 1; Length 193;
Best Local Similarity 77.7%; Pred. No. 1.4e-54;
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSLTRGL 96
QY 61 AVTISVKCEKISXLSCKENKIISFKENPPDNKDKTSIDIFFORSVPGHNDKNQFESSY 120
DB 97 AVTISVKCEKTSLSCKNKIISFKEMSPENINDEGNDIIFORSVPGHDKIQFESSLY 156
QY 121 EGYFLACERKDLFKLLKKEDELGRSMTFTVQNEED 157
DB 157 KGYFLACEKENDLFKLILKEKDEGDKSVMTVQNGN 193

Query Match 99.9%; Score 811; DB 1; Length 193;
Best Local Similarity 99.4%; Pred. No. 1e-68;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCKENKIISFKENPPDNKDKTSIDIFFORSVPGHNDKNQFESSY 120
DB 97 AVTISVKCEKISXLSCKENKIISFKENPPDNKDKTSIDIFFORSVPGHNDKNQFESSY 156
QY 121 EGYFLACERKDLFKLLKKEDELGRSMTFTVQNEED 157
DB 157 EGYFLACERKDLFKLLKKEDELGRSMTFTVQNEED 193

RESULT 2
IL18_HORSE STANDARD; PRT; 193 AA.
AC Q9XSG7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Argyle D.J., Penha-Goncalves M.N., Keanle J.L., Logan N.A.,
RA Nicolson L., Onions D.E.;
RA "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
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```

```
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CHAIN 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;

Query Match 81.2%; Score 659; DB 1; Length 193;
Best Local Similarity 77.7%; Pred. No. 1.4e-54;
Matches 122; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSLTRGL 96
QY 61 AVTISVKCEKISXLSCKENKIISFKENPPDNKDKTSIDIFFORSVPGHNDKNQFESSY 120
DB 97 AVTISVKCEKTSLSCKNKIISFKEMSPENINDEGNDIIFORSVPGHDKIQFESSLY 156
QY 121 EGYFLACERKDLFKLLKKEDELGRSMTFTVQNEED 157
DB 157 KGYFLACEKENDLFKLILKEKDEGDKSVMTVQNGN 193

RESULT 3
IL18_BOVIN STANDARD; PRT; 193 AA.
AC Q9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.;
RA "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RA 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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```
EMBL: AF124789; AAF08686.1; -
InterPro: IPR000975; Interleukin_1.
SMART: SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CHAIN 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 4.2e-54;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSLTRGL 96
```


[illegible]

RESULT 5

| | | | | |
|----|----------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------|------|---------|
| ID | IL18_CANFA | STANDARD; | PRT; | 193 AA. |
| AC | Q9XSRO; | | | |
| DT | 30-MAY-2000 | (Rel. 39, Created) | | |
| DT | 30-MAY-2000 | (Rel. 39, Last sequence update) | | |
| DT | 30-MAY-2000 | (Rel. 39, Last annotation update) | | |
| DE | Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor) (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma). | | | |
| GN | IL18 OR IGIF. | | | |
| OS | Canis familiaris (Dog). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. | | | |
| OX | NCBI_TaxID=9615; | | | |
| | [1] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RA | Argyle D.J., McGillivray C., Nicolson L., Onions D.E.; | | | |
| RT | "Cloning, sequencing and characterization of canine interleukin-18."; | | | |
| RL | Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases. | | | |
| CC | -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I CELLS (BY SIMILARITY). | | | |
| CC | -1- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY | | | |

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[illegible]

| | |
|------------|--------------------------------------------------------------------|
| RESULT 6 | |
| IL18_MOUSE | |
| ID | IL18_MOUSE |
| AC | P70380 |
| DT | 15-JUL-1998 (Rel. 36, Created) |
| DD | 15-JUL-1998 (Rel. 36, Last sequence update) |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) |
| DE | Interleukin-18 precursor (IL-18) Interferon-gamma inducing factor) |

```
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Tsutui H., Komatsu T., Yatsudo M., Hakura A.,
RA Tanimoto T., Torioka K., Okura T., Nukada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=NOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RA "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DR EMBL; D49949; BAA08705.1; -
DR EMBL; U66244; AAB49753.1; -
DR MGD; MGI:107936; IL18.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT VARSPLIC 183 185 MFT -> IS (IN REF. 2).
FT CONFLICT 183 185
FT CONFLICT 183 185
SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;

Query Match 63.4%; Score 515; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 3.7e-41;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGKLESLSVIRNLNDQVLFIDQGNRPFLFEDWTDSCRDNPRTIFIIISMYKDSQPRGMA 61
DB 37 FGRLHCTTAVIRINDQVLFVDK-RQVPFEDWTDIDQASAPQTRLIIIMYKDSEVRGLA 95
QY 62 VTISVCKEIKSLSCENKIISFKENPPDNKDKSDIIFFORSVPGHDNKMQFESSSYE 121
DB 96 VTLSVSKDGRMSTLSCNKKIISFEENPPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154
QY 122 GYFLACEKERDLFKLLKKKEDELDGRSINFTVQN 155
DB 155 GHFLACQKEDDAFKLLKKKDENGDKSVMTLTN 188

RESULT 7
IL18_RAT
ID IL18_RAT STANDARD; PRT: 194 AA.
AC P97636; P97637; O88749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
```

```
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=97152363; PubMed=8999896;
RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RT "Induction of interferon-gamma inducing factor in the adrenal
RT cortex.";
RL J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98368130; PubMed=9702748;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RA "Cloning of rat brain interleukin-18 cDNA.";
RL Mol. Psych. 3:362-365(1998).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77776; AAC53009.1; -
DR EMBL; U77777; AAC53010.1; -
DR EMBL; AJ222813; CAA11001.1; -
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
DR Cytokine; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
SQ SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;

Query Match 63.4%; Score 514.5; DB 1; Length 194;
Best Local Similarity 63.2%; Pred. No. 4.2e-41;
Matches 98; Conservative 28; Mismatches 28; Indels 1; Gaps 1;

QY 1 YFGKLESLSVIRNLNDQVLFIDQGNRPFLFEDWTDSCRDNPRTIFIIISMYKDSQPRGM 60
DB 37 HGRLHCTTAVIRINDQVLFVDKRNPPVFEEDMPDIDRTANESQTRLIIIMYKDSVGRGL 96
QY 61 AVTISVCKEIKSLSCENKIISFKENPPDNKDKSDIIFFORSVPGHDNKMQFESSSY 120
DB 97 AVTLSVSKDGRMSTLSCNKKIISFEENPPDENIDDIQSDLIFFQKRVPGH-NKMEFESSLY 155
QY 121 EGYFLACEKERDLFKLLKKKEDELDGRSINFTVQN 155
DB 156 GHFLACQKEDDAFKLLKKKDENGDKSVMTLTN 190

RESULT 8
IL1A_PIG
ID IL1A_PIG STANDARD; PRT: 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
```


| | | | |
|----|-----|---------------------------------------------------------------|-----|
| Db | 55 | -----GVFVHSLRSPNSRALSFK--LSAPOLLKREKVPDLPAYDLDLHLNLKK | 103 |
| QY | 101 | -----FFOR---SYP-GHDNKMQFESSYEGYFLACE--KERDLFKLT-----LKKDEELG | 145 |
| Db | 104 | PNQOFYANLISGVPAGKEGLSCFMCGLQKLYFNCNRPTELKLRILRLVTHWYQLCKE-KLG | 162 |
| QY | 146 | D 146 | |
| Db | 163 | D 163 | |

```

RESULT 13
Y414_MYCGE
ID Y414_MYCGE STANDARD; PRT; 1036 AA.
AC P47653; P47654; Q49457;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update),
DE Hypothetical protein MG414.
GN MG414.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RN Science 270:397-403(1995).
[2]
RP SEQUENCE OF 52-146 AND 733-833 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing.";
RN J. Bacteriol. 175:7918-7930(1993).
RL CC
CC -1- SIMILARITY: BELONGS TO THE MG414 / MG415 FAMILY.
-----
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[illegible]

DB 905 FIGVNDNQVESISY-----DLKITNNQTLIV-DANGFDNSINPDTIS-----EN 950
QY 130 ERDLFKLI---LKKDELGDRSFMFVQNEED 157
DB 951 OTQFLKALSFKYLNQNLQKRPVDFNLKSD 981

RESULT 14
CO3_MOUSE
ID CO3_MOUSE STANDARD; PRT: 1663 AA.
AC P01027;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Complement C3 precursor (HSE-MSF) [Contains: C3A anaphylatoxin].
GN C3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
C NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=85038854; PubMed=6208565;
RA Fey G.H., Lundwall A., Wetzel R.A., Tack B.F., de Bruijn M.H.L.,
RT Domdey H.;
RT "Nucleotide sequence of complementary DNA and derived amino acid
RT sequence of murine complement protein C3.";
RL Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:333-344(1984).
RN [2]
RP SEQUENCE OF 671-1663 FROM N.A. (LONG ISOFORM).
RX MEDLINE=85054819; PubMed=6094532;
RA Wetzel R.A., Lundwall A., Davidson F., Gibson T., Tack B.F., Fey G.H.;
RT "Structure of murine complement component C3. II. Nucleotide sequence
RT of cloned complementary DNA coding for the alpha chain.";
RL J. Biol. Chem. 259:13857-13862(1984).
RN [3]
RP SEQUENCE OF 671-748 FROM N.A.
RX MEDLINE=83117730; PubMed=6961437;
RA Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
RT "Characterization of the mRNA and cloned cDNA specifying the third
RT component of mouse complement.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623(1982).
RN [4]
RP SEQUENCE OF 658-761 FROM N.A.
RX MEDLINE=84201365; PubMed=6609661;
RA Fey G.H., Wiebauer K., Domdey H.;
RT "Amino acid sequences of mouse complement C3 derived from nucleotide
RT sequences of cloned cDNA.";
RL Ann. N.Y. Acad. Sci. 421:307-312(1983).
RN [5]
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=83117622; PubMed=6985486;
RA Wiebauer K., Domdey H., Diggelmann H., Fey G.;
RT "Isolation and analysis of genomic DNA clones encoding the third
RT component of mouse complement.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7077-7081(1982).
RN [6]
RP SEQUENCE OF 25-41 AND 749-760.
RX MEDLINE=93373334; PubMed=8364938;
RA Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.;
RT "A paracrine migration-stimulating factor for metastatic tumor cells
RT secreted by mouse hepatic sinusoidal endothelial cells:
RT Identification as complement component C3b.";
RL Cancer Res. 53:4418-4423(1993).
RN [7]
RP ALTERNATIVE INITIATION.
RX MEDLINE=95053742; PubMed=7964485;
RA Cahen-Kramer Y., Martensson I.L., Melchers F.;
RT "The structure of an alternate form of complement C3 that displays
RT costimulatory growth factor activity for B lymphocytes.";
RL J. Exp. Med. 180:2079-2088(1994).
CC -!- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE

COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE
THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
-!- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3.
C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
BASOPHILIC LEUKOCYTES. THE SHORT ISOFORM HAS B-CELL STIMULATORY
ACTIVITY.
-!- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
residues, forming two chains, beta and alpha, linked by a
disulfide bond. C3 convertase activates C3 by cleaving the alpha
chain, releasing C3A anaphylatoxin and generating C3B (beta chain
+ alpha' chain).
-!- ALTERNATIVE PRODUCTS: 2 isoforms: a long form (shown here) and a
short form; are produced by alternative initiation.
-!- MISCELLANEOUS: C3B IS RAPIDLY SPLIT IN TWO POSITIONS BY FACTOR I
AND A COFACTOR TO FORM IC3B (INACTIVATED C3B) AND C3F WHICH IS
RELEASED.
-!- MISCELLANEOUS: IC3B IS THE SLOWLY CLEAVED (POSSIBLY BY FACTOR I)
TO FORM C3C AND C3DG. OTHER PROTEASES PRODUCE OTHER FRAGMENTS SUCH
AS C3D OR C3G.
-!- SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
-!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.

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EMBL; K02782; AAC42013.1; -
EMBL; J00369; AAA37336.1; -
EMBL; J00367; AAA37336.1; JOINED.
EMBL; M33032; AAA37378.1; -
EMBL; Z37998; CAA86099.2; -
PIR; A05290; C3MS.
DR HSP; P01024; IC3D.
DR MGI; 88227; C3.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxn.
DR InterPro; IPR001599; MacrogloblnA2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01759; NTR; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01835; A2M_N; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2-MACROGLOBULIN; 1.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR Complement pathway; Complement alternate pathway; Plasma;
KW Inflammatory response; Glycoprotein; Signal; Alternative initiation.
FT SIGNAL 1 24
FT CHAIN 25 1663 COMPLEMENT C3.
FT CHAIN 25 666 COMPLEMENT C3, BETA CHAIN.
FT CHAIN 671 1663 COMPLEMENT C3, ALPHA CHAIN.
FT CHAIN 1129 1663 COMPLEMENT C3, SHORT ISOFORM.
FT INIT_MET 1129 1129 FOR SHORT ISOFORM.
FT PEPTIDE 671 748 C3A ANAPHYLATOXIN.
FT CHAIN 749 1663 C3B (ALPHA' CHAIN).
FT PEPTIDE 749 954 C3C FRAGMENT.
FT PEPTIDE 955 1303 C3DG FRAGMENT.
FT PEPTIDE 955 1001 C3G FRAGMENT.
FT PEPTIDE 1002 1303 C3D FRAGMENT.
FT PEPTIDE 1304 1320 C3F FRAGMENT.
FT SITE 748 749 CLEAVAGE (BY C3 CONVERTASE).

QY 1 YFGKLESKLSVIRNLNDQVL-----FIDQGNRPLFEDMTD-----SDCRDNAPR-TIFII 49
|: | | | : : : | | | | : : : | | | : : : | : : : :
Db 502 YYESLNKTLKKEVHEQLLSTEQVSDQKNAPAAESVSNNVTEYNSTLHENIKKQSLMML 561
QY 50 SMYKD---SOPRGMVTVISVCKEKISXL-SCENKI-----ISFKEMNPPDN---IKDTK 96
|: | : : : | | | : : : | | | : : : | : : : | : : : |
Db 562 QMFEDLHIOESKINNLTVSLMEKEKESLRGECEMDLSKCRNDFKQLKDTENLHVLNQT 621
QY 97 SDIIFQRSVPGHDKM-----QFESSYE 121
|: | : : : | | | | : : : | : : : | : : : | : : : |
Db 622 AEVL-----PMDNKMSEQLNDLTYD 645

Search completed: April 4, 2003, 10:59:50
Job time : 14 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 4, 2003, 10:57:21 ; Search time 85 seconds
(without alignments)
380.581 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 798 | 98.3 | 193 | 4 Q96KJ8 | Q96KJ8 homo sapien |
| 2 | 792 | 97.5 | 193 | 6 Q9BG15 | Q9BG15 macaca mula |
| 3 | 654 | 80.5 | 178 | 6 Q9MZ18 | Q9MZ18 bos taurus |
| 4 | 648 | 79.8 | 193 | 6 Q9GL09 | Q9GL09 ovis aries |
| 5 | 634 | 78.1 | 192 | 6 Q9SM33 | Q9SM33 felis silve |
| 6 | 626 | 77.1 | 192 | 6 Q9N1P7 | Q9N1P7 sus scrofa |
| 7 | 441 | 54.3 | 196 | 11 Q91Z66 | Q91Z66 sigmodon hi |
| 8 | 313 | 38.5 | 84 | 6 Q95LE7 | Q95LE7 canis fami |
| 9 | 204 | 25.1 | 45 | 4 Q9NQ49 | Q9NQ49 homo sapien |
| 10 | 193 | 23.8 | 211 | 13 Q98S01 | Q98S01 anas platyr |
| 11 | 182.5 | 22.5 | 198 | 13 Q918D2 | Q918D2 gallus gall |
| 12 | 178.5 | 22.0 | 196 | 13 Q8QF08 | Q8QF08 gallus gall |
| 13 | 88 | 10.8 | 4643 | 5 Q9VW71 | Q9VW71 drosophila |
| 14 | 85 | 10.5 | 381 | 3 Q43031 | Q43031 schizosacch |
| 15 | 82 | 10.1 | 263 | 3 Q74316 | Q74316 schizosacch |
| 16 | 82 | 10.1 | 1501 | 5 Q22699 | Q22699 caenorhabdi |

Q25986 plasmodium
Q93kf0 caldicellul
Q84500 chlamydia t
Q8xj13 clostridium
Q9sdm4 dunaliella
Q94173 pneumocysti
Q25249 helicobacte
Q9znj7 clostridium
Q16673 caenorhabdi
Q91365 coturnix co
Q9pm33 campylobact
Q9bgdl microrycter
Q9qba2 yaba monkey
Q8s484 zea mays (m
Q80569 arabidopsis
Q8ry34 arabidopsis
Q82393 arabidopsis
Q9nuci homo sapien
Q8xk91 clostridium
Q77077 plasmodium
Q8vi98 mus musculo
Q8sv24 encephalito
Q9bge4 erophylla s
Q9bga8 sturnira li
Q8u2pi pyrococcus
Q90601 gallus gall
Q95qv2 caenorhabdi
Q90681 gallus gall
Q9zsb9 arabidopsis

ALIGNMENTS

RESULT 1

Q96KJ8 ID Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF380360; AAK57024.1; ...
SQ SEQUENCE 193 AA; 22323 MW; 2B500205D1B7E5F7 CRC64;

Query Match 98.3%; Score 798; DB 4; Length 193;
Best Local Similarity 97.5%; Pred. No. 1.2e-71;
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 60
Db 37 YFGKLESKLSVIRNLNDQVLFDQGNRPLFEDMTSDCRDNAPRTFIISMYKDSQPRGM 96
Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQFORSVPGHDKMKQFESSY 120
Db 97 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQFORSVPGHDKMKQFESSY 156

Qy 121 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNE 157
Db 157 EGYFLACERDLFKLILKKKEDELGDRSIMFTVQNE 193

RESULT 2

Q9BG15

```

ID Q9BG15 PRELIMINARY; PRT; 193 AA.
AC Q9BG15;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18.
GN IL18.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21229850; PubMed=11331040;
RA Glavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result in Increased Viral
RT Replication.";
DT J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL: AF303732; AAK13416.1; -.
SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;

Query Match 97.5%; Score 792; DB 6; Length 193;
Best Local Similarity 95.5%; Pred. No. 4.8e-71;
Matches 150; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIINMYKDSQPRGM 96
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
DB 97 AVAISVKCEKISTLSCENRIISFKEMNPPDNIDKTSDIIFQSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLFKLILKKKDELGRSINFTVQNEED 157
DB 157 EGYFLACEKERDLFKLILKKKDELGRSINFTVQNEED 193

RESULT 3
Q9WZL8 PRELIMINARY; PRT; 178 AA.
AC Q9WZL8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY, LIVER, AND BLOOD;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrl M., Bolin C.A.;
RT "Cloning of bovine Interleukin-18, expression in Escherichia coli, and
RT characterization of the biologic activities of the recombinant
RT cytokine.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF173175; AAF89833.1; -.
DR InterPro: IPR000975; Interleukin_1.
DE SMART: SM00125; IL1; 1.
FT NON_TER 1 178
FT NON_TER 178 178
SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match 80.5%; Score 654; DB 6; Length 178;
Best Local Similarity 77.1%; Pred. No. 2.3e-57;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

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```

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 22 HFQKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIVYKDSLTRL 81
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
DB 82 AVTISVQCKKMTSLSCENKIISFKEMNPPDNIDNEESDIIFQSVPGHDKIQFESSLY 141
QY 121 EGYFLACEKERDLFKLILKKKDELGRSINFTVQNEED 157
DB 142 KGFLACKKENDLFKLILKKQDDNRDKSVNFTVQNN 178

RESULT 4
Q9GL09 PRELIMINARY; PRT; 193 AA.
AC Q9GL09;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18 (IGIF).
GN IL-18.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT "Cloning of Ovine Interleukin 18 cDNA.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ401033; CAC09326.2; -.
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 79.8%; Score 648; DB 6; Length 193;
Best Local Similarity 77.7%; Pred. No. 1e-56;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
DB 37 HFQKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIIVYKDSLTRL 96
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIDKTSDIIFQSVPGHDKMKQFESSY 120
DB 97 AVTISVQCKKMTSLSCENKIISFKEMNPPDNIDNEESDIIFQSVPGHDKIQFESSLY 156
QY 121 EGYFLACEKERDLFKLILKKKDELGRSINFTVQNEED 157
DB 157 KGFLACKKENDLFKLILKKQDDNRDKSVNFTVQNN 193

RESULT 5
Q95W33 PRELIMINARY; PRT; 192 AA.
AC Q95W33;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interferon-gamma inducing factor.
GN IGIF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;
RT "Nucleotide sequence of feline IGIF cDNA (provisional).";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y13923; CAC42918.1; -.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Farhan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ295724; CAC01436.1; -
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.1%; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTDSDCR 39
   |||||
7 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTDSDCR 45

RESULT 10
Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF361622; AAK26322.1; -
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.8%; Score 193; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 2e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGLKESKLSVIRNLNDQVLFIDQGNRPDPEDMTDSDCRNAPRTIFIISMYKDSQP-RG 59
   |||||
43 FSKEKTLHRLNRVNSQVLRVLPDLNVAAPEDVDQEMKSGSGMN-FCMHYKTTTPSAG 101
   |||||
60 MAVTISVKCE-KISXLSCEK-----IISFKEMNPPDNKDTKSDIIFFORSVPGHDNK-M 113
   |||||
102 MPVAFSVRVEDKSYVMCEEHGKMIVRFREGEVPKDIPG-ESNIIFFKTTFSYSSKAF 160
   |||||
114 QFESSSVYEGFLACERDLFKLILKK---EDELGDRS-IMFTVQNE 156
   |||||
161 KFEYSLERGMFLAFEEEDSLRKLILKKLPREDEVDETTKITLTSHNE 207

RESULT 11
Q918D2 PRELIMINARY; PRT; 198 AA.
AC Q918D2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 18.
GN IL-18.
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OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20508574; PubMed-11054275;
RA Schneider K., Puehler F., Baeuerle D., Elvers S., Staeheli P.,
RA Kaspers B., Weining K.C.;
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL: AJ277865; CAB96214.1; -
FT CHAIN 30
FT CHAIN 198
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;
Best Local Similarity 36.8%; Pred. No. 2.1e-10;
Matches 57; Conservative 25; Mismatches 60; Indels 13; Gaps 7;

QY 13 RNLDNDQVLFIDQGNRPDPEDMTDSDCRNAPRTIFIISMYKDSQP-RGMVATISVKCEK 70
   |||||
42 RNVNSQLLVVVRPDLNVAAPEDVDQEVKSGS-GMYFDHCYKTAPSAGMPVAFSVQVED 100
   |||||
71 ISXLSCEK-----IISFKEMNPPDNKDTKSDIIFFORSVPGHDNK-MQFESSSVYEGYF 124
   |||||
101 KSYVMCEEHGKMVRFREGEVPKDIPG-ESNIIFFKTTFTSCSKAFKFEYSLEQGMF 159
   |||||
125 LACEKERDLFKLILKK---EDELGDRS-IMFTVQNE 156
   |||||
160 LAFEEEDSLRKLILKKLPREDEVDETTKFVTSHNE 194

RESULT 12
Q8QF08 PRELIMINARY; PRT; 196 AA.
AC Q8QF08;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interleukin-18 precursor.
GN IL18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Rothwell L., Buerstedde J.M., Kaiser P.;
RT "Cloning and characterisation of chicken interleukin-18.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ276025; CAC81652.1; -
KW Signal.
FT SIGNAL 1
FT SIGNAL 29
FT CHAIN 30
FT CHAIN 196
SQ SEQUENCE 196 AA; 22787 MW; 4947DECCB92414 CRC64;

Query Match 22.0%; Score 178.5; DB 13; Length 196;
Best Local Similarity 34.3%; Pred. No. 5.1e-10;
Matches 60; Conservative 26; Mismatches 68; Indels 21; Gaps 8;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPDPEDMTDSDCRNAPRTIFIIS 51
   |||||
20 YFEECEDAFCKDKTKRFRFRNVNSQLLVVVRPDLNVAAPEDVDQEVKSGS-GMYEDIHC 78
   |||||
52 YKDSQPRG-MAVTISVKCEKISXLSCEK-----IISFKEMNPPDNKDTKSDIIFFORS 105
   |||||
79 YKTTAPSARMPVAFSVQVEDKSYVMCEEHGKMVRFREGEVPKDIPG-ESNIIFFKTT 137
   |||||
106 VPGHDNK-MQFESSSVYEGFLACERDLFKLILKK---EDELGDRS-IMFTVQNE 156
   |||||
138 FTSCSKAFKFEYSLEQGMFLAFEEEDSLRKLILKKLPREDEVDETTKFVTSHNE 192
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RESULT 13
Q9VW71
ID Q9VW71 PRELIMINARY; PRT: 4643 AA.
AC Q9VW71
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE putative fat-like cadherin precursor (CG7749 protein).
GN CG7749
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista A.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT *The genome sequence of Drosophila melanogaster.*;
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
CC -1- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAIN.
DR EMBL: AE003515; AAF49078.1; -
DR HSSP: P15116; INCI.
DR Flybase: FBgn0036930; fat2.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR001791; Laminin_G.
DR Pfam: PF00028; cadherin; 31.
DR Pfam: PF00008; EGF; 5.
DR Pfam: PF00054; laminin_G; 1.
DR PRINTS: PRO0205; CADHERIN.
DR SMART: SM00112; CA; 33.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 5.
DR SMART: SM00282; LamG; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00232; CADHERIN_1; 17.
DR PROSITE: PS00268; CADHERIN_2; 41.
DR PROSITE: PS00022; EGF_1; 5.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR Hypothetical protein; Cell adhesion; Signal; Transmembrane; Repeat;
KW EGF-like domain; Glycoprotein; Calcium-binding.
FT SIGNAL 1 35
FT CHAIN 36 4643 PUTATIVE FAT-LIKE CADHERIN.
FT DOMAIN 36 1647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1648 1668 POTENTIAL.
FT DOMAIN 1669 4643 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 68 180 CADHERIN 1.
FT DOMAIN 189 288 CADHERIN 2.
FT DOMAIN 293 397 CADHERIN 3.
FT DOMAIN 406 504 CADHERIN 4.
FT DOMAIN 513 610 CADHERIN 5.
FT DOMAIN 619 713 CADHERIN 6.
FT DOMAIN 778 874 CADHERIN 7.
FT DOMAIN 883 977 CADHERIN 8.
FT DOMAIN 986 1085 CADHERIN 9.
FT DOMAIN 1094 1190 CADHERIN 10.
FT DOMAIN 1199 1296 CADHERIN 11.
FT DOMAIN 1305 1402 CADHERIN 12.
FT DOMAIN 1413 1503 CADHERIN 13.
FT DOMAIN 1512 1609 CADHERIN 14.
FT DOMAIN 1618 1714 CADHERIN 15.
FT DOMAIN 1723 1812 CADHERIN 16.
FT DOMAIN 1821 1929 CADHERIN 17.
FT DOMAIN 1948 2030 CADHERIN 18.
FT DOMAIN 2024 2137 CADHERIN 19.
FT DOMAIN 2146 2232 CADHERIN 20.
FT DOMAIN 2247 2338 CADHERIN 21.
FT DOMAIN 2347 2465 CADHERIN 22.
FT DOMAIN 2474 2567 CADHERIN 23.
FT DOMAIN 2576 2670 CADHERIN 24.
FT DOMAIN 2679 2779 CADHERIN 25.
FT DOMAIN 2788 2876 CADHERIN 26.
FT DOMAIN 2885 2983 CADHERIN 27.
FT DOMAIN 2992 3083 CADHERIN 28.
FT DOMAIN 3092 3185 CADHERIN 29.
FT DOMAIN 3194 3289 CADHERIN 30.
FT DOMAIN 3298 3394 CADHERIN 31.
FT DOMAIN 3403 3499 CADHERIN 32.
FT DOMAIN 3508 3604 CADHERIN 33.
FT DOMAIN 3618 3671 CADHERIN 34.
FT DOMAIN 3819 3879 EGF-LIKE 1.
FT DOMAIN 3881 3919 EGF-LIKE 2.
FT DOMAIN 4129 4166 EGF-LIKE 3.
FT DOMAIN 4168 4205 EGF-LIKE 4.
FT DOMAIN 4243 4279 EGF-LIKE 5.
FT DISULFID 3823 3835 POTENTIAL.
FT DISULFID 3830 3867 POTENTIAL.
FT DISULFID 3869 3878 POTENTIAL.
FT DISULFID 3885 3896 POTENTIAL.
FT DISULFID 3890 3907 POTENTIAL.
FT DISULFID 3909 3918 POTENTIAL.
FT DISULFID 4133 4144 POTENTIAL.
FT DISULFID 4156 4165 POTENTIAL.
FT DISULFID 4172 4183 POTENTIAL.
FT DISULFID 4177 4193 POTENTIAL.
FT DISULFID 4195 4204 POTENTIAL.
FT DISULFID 4247 4258 POTENTIAL.
FT DISULFID 4252 4267 POTENTIAL.
FT DISULFID 4269 4278 POTENTIAL.

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FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 779 779 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 843 843 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1106 1106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1312 1312 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1439 1439 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1511 1511 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 4643 AA; 51614 MW; 7EC52BD36ADD4E89 CRC64;

Query Match 10.8%; Score 88; DB 5; Length 4643;
Best Local Similarity 23.6%; Pred. No. 18;
Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;

QY 32 DMTDSCDRNAPRTIFIISMV-----KDSQPRGMATISVKCEKISXLSNCKIISF--KE 85
DB 2124 DISVLVDNDNCP--LFVNMPYATVSIDDPKG---TIIMQVKAIDLDSAENGVRVELKK 2178
QY 86 MNPPDNKIKTSDIIFQSRVPHGDKMKQFESSYEGYFLACEKERDL----- 133
DB 2179 NGELFKLDRKSGELSIKQHVGHNRNYELTVAAYDGAITPCSEAPLQVKVIDRSMVPV 2238
QY 134 ---FKILKKED-----ELGDRSIMFTVONE 156
DB 2239 EKQFYIVSVKEDVMYSALVSIEASPLG--RSLIITISSE 2278

RESULT 14
ID 043031 PRELIMINARY; PRT; 381 AA.
AC 043031; Q9US93;
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE Hypothetical 44.2 kDa protein C3B9.02C in chromosome II.
GN SPBC3B9.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022070; CAAL7782.1; -.
DR EMBL; AB027944; BAA87248.1; -.
DR InterPro; IPR000457; G_patch.
DR SMART; SM00443; G_patch; 1.
DR Hypothetical protein.
SQ SEQUENCE 381 AA; 44214 MW; E1542538B667549F CRC64;

Query Match 10.5%; Score 85; DB 3; Length 381;
Best Local Similarity 26.4%; Pred. No. 2.1;
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;

QY 3 GKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMVKDSQPRGMAT 62
DB 208 GQLSSKDAF--DVNQRPFLGCAKPVDSSELTETLDIWKNPCKTWF----- 250
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QY 63 TISVK-CEKISXLSNCKIISF-KENPPDNKIKTSDIIFQSRVPHGDKMKQFESSY 120
DB 251 -LPVKPLESNALSNQHEUTEVQKNSIDNL--TPSELFRKRS---RDNNLSRESS-- 302
QY 121 EGYFLACEKERDLFKLLKKKEDELGDGRS 148
DB 303 -----VSSKHLDYNSRNYKRRDRDPRT 325

RESULT 15
ID 074316 PRELIMINARY; PRT; 263 AA.
AC 074316;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 30.3 kDa protein.
GN SPBC15D4.11C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Lyne M., Rajandream M.A., Barrell B.G., Lucas M., Gaillardin C.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031349; CAA20486.2; -.
DR InterPro; IPR003428; MAM33.
DR Pfam; PF02330; MAM33; 1.
SQ SEQUENCE 263 AA; 30254 MW; F5673E959584C99B CRC64;

Query Match 10.1%; Score 82; DB 3; Length 263;
Best Local Similarity 21.7%; Pred. No. 2.8;
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;

QY 4 KLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRNAPRTIFIISMVKDSQPRGMAT 63
DB 47 KLDSELGYVKQVLDLTPKKGYEKALHSFIHED-----PSLNYISALKETAKIRVT 100
QY 64 ISVKCEKISXLSNCKIISF-KENPPDNKIKTSDIIFQSRVPHG----- 109
DB 101 VPVYSRKSYV--QTKPITHSAEN--ENGNETSDELVFFQHSIPAYVQLTNNHGTILCAL 156
QY 110 ---DNKMQFESSYEGYFLACEKERDLFKLLKKKEDELGDGR 147
DB 157 ILCKGMLHFDSTISFQSPQNSQAFSSDL-RLILOKSKYTCR 196

Search completed: April 4, 2003, 11:01:23
Job time : 88 secs
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